

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2004, 03:11:30 ; Search time 7823 Seconds
(without alignments)
11418.892 Million cell updates/sec

Title: US-09-930-591-1

Perfect score: 2061

Sequence: 1 atggcgctatcacggccta.....atgaaatggaagagtgtga 2061

Scoring table: OLIGO NUC
Gapop 60.0, Gapext 60.0

Searched: 3470272 seqs, 21671516995 residues

Word size : 35 *or more*

Total number of hits satisfying chosen parameters: 311

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pln.*
- 35: em.htg.rod.*
- 36: em.htg.man.*
- 37: em.htg.vrt.*
- 38: em.sy.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2061	100.0	2061	6	AX441176	AX441176 Sequence
2	2061	100.0	2061	6	AX467113	AX467113 Sequence
3	92	4.5	9610	14	HEC278830	AJ278830 Hepatitis
4	76	3.7	9426	14	AF511949	AF511949 Hepatitis
5	62	3.0	943	6	A22779	A22779 non-structu
6	62	3.0	943	6	AR031209	AR031209 Sequence
7	62	3.0	943	6	AR145025	AR145025 Sequence
8	62	3.0	943	6	HPCNS3NS4	DI0664 Hepatitis C
9	62	3.0	9365	14	AF290978	AF290978 Hepatitis
10	62	3.0	9395	14	AF511950	AF511950 Hepatitis
11	61	3.0	957	6	BD226202	BD226202 Improved
12	59	2.9	241	14	HPCNS10CLN	M94401 Hepatitis C
13	59	2.9	241	14	HPCNS11CLN	M94400 Hepatitis C
14	59	2.9	550	14	HCVNSTP	X71406 Hepatitis C
15	59	2.9	1477	14	HPCNS34	M60220 Hepatitis C
16	58	2.8	382	6	AR124773	AR124773 Sequence
17	58	2.8	382	6	AR353560	AR353560 Sequence
18	58	2.8	1414	6	AR124772	AR124772 Sequence
19	58	2.8	1414	6	AR353559	AR353559 Sequence
20	58	2.8	1420	6	AR124774	AR124774 Sequence
21	58	2.8	1420	6	AR353561	AR353561 Sequence
22	57	2.8	162	14	HPCNS35	M55151 Hepatitis C
23	57	2.8	223	14	HPCNS17CLN	M94451 Hepatitis C
24	57	2.8	229	14	HPCNS15CLN	M94449 Hepatitis C
25	57	2.8	241	14	HPCNSCLN5	M94469 Hepatitis C
26	56	2.7	281	6	I32190	I32190 Sequence 75
27	56	2.7	281	6	I34281	I34281 Sequence 75
28	56	2.7	281	6	I82486	I82486 Sequence 75
29	56	2.7	281	6	BD140411	BD140411 Hepatitis
30	56	2.7	283	6	AR118676	AR118676 Sequence
31	56	2.7	368	6	I32188	I32188 Sequence 71
32	56	2.7	368	6	I34279	I34279 Sequence 71
33	56	2.7	368	6	I82484	I82484 Sequence 71
34	56	2.7	368	6	BD140409	BD140409 Hepatitis
35	56	2.7	543	14	AF369231	AF369231 Hepatitis
36	56	2.7	1284	14	HPCNS3PROB	M62386 Hepatitis C
37	56	2.7	2058	6	AR404933	AR404933 Sequence
38	56	2.7	2058	6	AR408362	AR408362 Sequence
39	56	2.7	2058	6	AX395309	AX395309 Sequence
40	56	2.7	2058	6	AX454818	AX454818 Sequence
41	56	2.7	2064	6	I32187	I32187 Sequence 69
42	56	2.7	2064	6	I34278	I34278 Sequence 69
43	56	2.7	2064	6	I82483	I82483 Sequence 69
44	56	2.7	2064	6	BD140408	BD140408 Hepatitis
45	56	2.7	2283	6	BD140416	BD140416 Hepatitis
46	56	2.7	2523	6	I32195	I32195 Sequence 85
47	56	2.7	2523	6	I34286	I34286 Sequence 85
48	56	2.7	2523	6	I82491	I82491 Sequence 85
49	56	2.7	5360	6	AR118686	AR118686 Sequence
50	56	2.7	5360	6	I06434	I06434 Sequence 48
51	56	2.7	5360	6	I09328	I09328 Sequence 8
52	56	2.7	6299	6	AX164584	AX164584 Sequence
53	56	2.7	6785	6	AR118692	AR118692 Sequence
54	56	2.7	6785	6	I06440	I06440 Sequence 54
55	56	2.7	6785	6	I09329	I09329 Sequence 10
56	56	2.7	7310	6	AR118696	AR118696 Sequence
57	56	2.7	7310	6	I09331	I09331 Sequence 15
58	56	2.7	7310	14	HPCPOLYP	M32084 Hepatitis C
59	56	2.7	8316	6	AR118703	AR118703 Sequence
60	56	2.7	8987	6	AR118728	AR118728 Sequence
61	56	2.7	9185	6	AR118722	AR118722 Sequence
62	56	2.7	9185	6	AR118723	AR118723 Sequence
63	56	2.7	9185	6	I08294	I08294 Sequence 1
64	56	2.7	9185	6	BD091382	BD091382 HCV culti
65	56	2.7	9379	6	AR118747	AR118747 Sequence

66	56	2.7	9379	6	AR166930	Sequence	139	48	2.3	6935	14	HPCT2	D16435	Hepatitis C
67	56	2.7	9379	6	AR301300	Sequence	140	48	2.3	9033	14	D89872	D89872	Hepatitis C
68	56	2.7	9401	6	AR176483	Sequence	141	48	2.3	9379	14	AF207765	AF207765	Hepatitis C
69	56	2.7	9401	6	E66593	Hepatitis C	142	48	2.3	9427	14	HPCURNA	D14484	Hepatitis C
70	56	2.7	9401	6	I71894	Sequence 9	143	48	2.3	9434	14	HPCUTB	D11355	Hepatitis C
71	56	2.7	9401	6	I71885	Sequence 9	144	48	2.3	9436	6	E07266	E07266	Blood-splea
72	56	2.7	9401	6	BD080334	Hepatitis C	145	48	2.3	9436	14	HPCUTB	D11168	Hepatitis C
73	56	2.7	9401	14	HPCLYPRE	M62321	146	47	2.3	232	14	HPCNS7CLN	M94411	Hepatitis C
74	56	2.7	9609	12	AF387805	Synthetic	147	47	2.3	241	14	HPCNS4CLN	M94402	Hepatitis C
75	56	2.7	9609	12	AF387808	Synthetic	148	47	2.3	543	14	AF369232	AF369232	Hepatitis C
76	56	2.7	9646	12	AF387806	Synthetic	149	47	2.3	543	14	AF369241	AF369241	Hepatitis C
77	56	2.7	9693	12	AF387807	Synthetic	150	47	2.3	543	14	AF369242	AF369242	Hepatitis C
78	55	2.7	543	14	AF369219	Hepatitis C	151	47	2.3	543	14	AF369243	AF369243	Hepatitis C
79	53	2.6	414	14	HCU14261	U14261	152	47	2.3	543	14	AF369243	AF369243	Hepatitis C
80	53	2.6	475	6	AX361030	Sequence	153	47	2.3	9502	6	E08263	E08263	grNA of Hep
81	53	2.6	475	6	AX361032	Sequence	154	47	2.3	9502	6	E08264	E08264	cDNA of Hep
82	53	2.6	583	6	AX361032	Sequence	155	44	2.1	9502	6	E08264	E08264	cDNA of Hep
83	53	2.6	583	6	AX361032	Sequence	156	44	2.1	9502	6	E08264	E08264	cDNA of Hep
84	53	2.6	585	14	S68681	putative no	157	44	2.1	9502	6	E08264	E08264	cDNA of Hep
85	53	2.6	790	6	AX361031	Sequence	158	44	2.1	9502	6	E08264	E08264	cDNA of Hep
86	53	2.6	790	6	AX361031	Sequence	159	44	2.1	9502	6	E08264	E08264	cDNA of Hep
87	53	2.6	836	6	AX361029	Sequence	160	44	2.1	9502	6	E08264	E08264	cDNA of Hep
88	53	2.6	836	6	AX361029	Sequence	161	44	2.1	9502	6	E08264	E08264	cDNA of Hep
89	53	2.6	1284	14	HPCCGAA	M62385	162	44	2.1	9502	6	E08264	E08264	cDNA of Hep
90	53	2.6	9416	6	AX361031	Sequence	163	44	2.1	9502	6	E08264	E08264	cDNA of Hep
91	53	2.6	9518	6	AX100563	Sequence	164	44	2.1	9502	6	E08264	E08264	cDNA of Hep
92	53	2.6	9518	6	AX100563	Sequence	165	44	2.1	9502	6	E08264	E08264	cDNA of Hep
93	53	2.6	9599	6	AR119831	Sequence	166	44	2.1	9502	6	E08264	E08264	cDNA of Hep
94	53	2.6	9599	6	AR119831	Sequence	167	44	2.1	9502	6	E08264	E08264	cDNA of Hep
95	53	2.6	9599	14	AF011751	AF011751	168	44	2.1	9502	6	E08264	E08264	cDNA of Hep
96	53	2.6	9599	14	AF011752	AF011752	169	44	2.1	9502	6	E08264	E08264	cDNA of Hep
97	53	2.6	9599	14	AF011753	AF011753	170	44	2.1	9502	6	E08264	E08264	cDNA of Hep
98	53	2.6	9611	6	AX057088	AX057088	171	44	2.1	9502	6	E08264	E08264	cDNA of Hep
99	53	2.6	9611	6	AX057092	AX057092	172	44	2.1	9502	6	E08264	E08264	cDNA of Hep
100	53	2.6	9611	6	AX057094	AX057094	173	44	2.1	9502	6	E08264	E08264	cDNA of Hep
101	53	2.6	9611	14	AF177037	AF177037	174	44	2.1	9502	6	E08264	E08264	cDNA of Hep
102	53	2.6	9611	14	AF177038	AF177038	175	44	2.1	9502	6	E08264	E08264	cDNA of Hep
103	53	2.6	9611	14	AF177039	AF177039	176	44	2.1	9502	6	E08264	E08264	cDNA of Hep
104	53	2.6	9611	14	AF177040	AF177040	177	44	2.1	9502	6	E08264	E08264	cDNA of Hep
105	53	2.6	9611	14	AF177040	AF177040	178	44	2.1	9502	6	E08264	E08264	cDNA of Hep
106	53	2.6	9646	6	BD069982	BD069982	179	44	2.1	9502	6	E08264	E08264	cDNA of Hep
107	53	2.6	9646	14	AF009606	AF009606	180	44	2.1	9502	6	E08264	E08264	cDNA of Hep
108	53	2.6	9646	14	AF009606	AF009606	181	44	2.1	9502	6	E08264	E08264	cDNA of Hep
109	53	2.6	12980	6	AR110831	AR110831	182	44	2.1	9502	6	E08264	E08264	cDNA of Hep
110	53	2.6	12980	6	BD069985	BD069985	183	44	2.1	9502	6	E08264	E08264	cDNA of Hep
111	52	2.5	885	6	AX48835	AX48835	184	44	2.1	9502	6	E08264	E08264	cDNA of Hep
112	52	2.5	885	6	AR104893	AR104893	185	44	2.1	9502	6	E08264	E08264	cDNA of Hep
113	52	2.5	885	6	AR163011	AR163011	186	44	2.1	9502	6	E08264	E08264	cDNA of Hep
114	52	2.5	885	6	AR173561	AR173561	187	44	2.1	9502	6	E08264	E08264	cDNA of Hep
115	52	2.5	885	6	AX774443	AX774443	188	44	2.1	9502	6	E08264	E08264	cDNA of Hep
116	52	2.5	885	6	BD132062	BD132062	189	44	2.1	9502	6	E08264	E08264	cDNA of Hep
117	50	2.4	337	6	AX360976	AX360976	190	44	2.1	9502	6	E08264	E08264	cDNA of Hep
118	50	2.4	337	6	AX377642	AX377642	191	44	2.1	9502	6	E08264	E08264	cDNA of Hep
119	50	2.4	373	6	AR230498	AR230498	192	44	2.1	9502	6	E08264	E08264	cDNA of Hep
120	50	2.4	373	6	AR310193	AR310193	193	44	2.1	9502	6	E08264	E08264	cDNA of Hep
121	50	2.4	373	6	AX350605	AX350605	194	44	2.1	9502	6	E08264	E08264	cDNA of Hep
122	50	2.4	442	6	AX360964	AX360964	195	44	2.1	9502	6	E08264	E08264	cDNA of Hep
123	50	2.4	442	6	AX377630	AX377630	196	44	2.1	9502	6	E08264	E08264	cDNA of Hep
124	50	2.4	543	14	AF369214	AF369214	197	44	2.1	9502	6	E08264	E08264	cDNA of Hep
125	50	2.4	543	14	AF369227	AF369227	198	44	2.1	9502	6	E08264	E08264	cDNA of Hep
126	50	2.4	543	14	AF369230	AF369230	199	44	2.1	9502	6	E08264	E08264	cDNA of Hep
127	50	2.4	543	14	AF369233	AF369233	200	44	2.1	9502	6	E08264	E08264	cDNA of Hep
128	50	2.4	543	14	AF369235	AF369235	201	44	2.1	9502	6	E08264	E08264	cDNA of Hep
129	50	2.4	543	14	AF369237	AF369237	202	44	2.1	9502	6	E08264	E08264	cDNA of Hep
130	50	2.4	559	6	AX361034	AX361034	203	44	2.1	9502	6	E08264	E08264	cDNA of Hep
131	50	2.4	559	6	AX377700	AX377700	204	44	2.1	9502	6	E08264	E08264	cDNA of Hep
132	50	2.4	617	6	AX361033	AX361033	205	44	2.1	9502	6	E08264	E08264	cDNA of Hep
133	50	2.4	617	6	AX377699	AX377699	206	44	2.1	9502	6	E08264	E08264	cDNA of Hep
134	50	2.4	1251	6	AR124766	AR124766	207	44	2.1	9502	6	E08264	E08264	cDNA of Hep
135	50	2.4	1251	6	AR353553	AR353553	208	44	2.1	9502	6	E08264	E08264	cDNA of Hep
136	50	2.4	9424	14	AF511948	AF511948	209	44	2.1	9502	6	E08264	E08264	cDNA of Hep
137	48	2.3	5211	6	BD270487	BD270487	210	44	2.1	9502	6	E08264	E08264	cDNA of Hep
138	48	2.3	5211	6	AX044453	AX044453	211	44	2.1	9502	6	E08264	E08264	cDNA of Hep

/db_xref="taxon:32630" /note="Hepatitis C virus NS3/4A coding region"									
ORIGIN									
Query Match 100.0%; Score 2061; DB 6; Length 2061; Best Local Similarity 100.0%; Pred. No. 0; Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	ATGGCGCTATCAGCGCTATGCCAGCAGACAAGGGGCTTTGGGATGATTAATCACC	60						
DB	1	ATGGCGCTATCAGCGCTATGCCAGCAGACAAGGGGCTTTGGGATGATTAATCACC	60						
QY	61	AGCTTGACCGCGCGGAGAAAAACAGGTGAGAGTGAAGTTCAGATCGTGAACGTCT	120						
DB	61	AGCTTGACCGCGCGGAGAAAAACAGGTGAGAGTGAAGTTCAGATCGTGAACGTCT	120						
QY	121	GCCAGACATTCTTGGCAACTGCTAATAACGGGTGTGTTGGACTGTACCAATGGAGCC	180						
DB	121	GCCAGACATTCTTGGCAACTGCTAATAACGGGTGTGTTGGACTGTACCAATGGAGCC	180						
QY	181	GGAAACAGGACCATTCGTACCTAAGGTCTCTGTTATCCAGATGTACCAATGGAGCC	240						
DB	181	GGAAACAGGACCATTCGTACCTAAGGTCTCTGTTATCCAGATGTACCAATGGAGCC	240						
QY	241	CAAGACCTCGTAGGCTGGCGGCTCCCAAGGTGCCCGCTCAITTAACACCATGCACTTGC	300						
DB	241	CAAGACCTCGTAGGCTGGCGGCTCCCAAGGTGCCCGCTCAITTAACACCATGCACTTGC	300						
QY	301	GGCTCCTCGACCTTACCTGTCACGAGGACGCGCGATGTCATTCCTGTCGCGCCACGG	360						
DB	301	GGCTCCTCGACCTTACCTGTCACGAGGACGCGCGATGTCATTCCTGTCGCGCCACGG	360						
QY	361	GCTGATGGAGGGCAGCGCTTTCGCCCGCGCTATCTTACCTGTAAGGCTCCTCG	420						
DB	361	GCTGATGGAGGGCAGCGCTTTCGCCCGCGCTATCTTACCTGTAAGGCTCCTCG	420						
QY	421	GGAGGCTCTGTGTCGCCCGCAGGACATCCCGTAGGCATATTCAGAGCGCGGTATGC	480						
DB	421	GGAGGCTCTGTGTCGCCCGCAGGACATCCCGTAGGCATATTCAGAGCGCGGTATGC	480						
QY	481	ACCGTGGAGTGGCTAAGGGGTGGACTTCATCCCGTAGAGCTTAGAGACAACATG	540						
DB	481	ACCGTGGAGTGGCTAAGGGGTGGACTTCATCCCGTAGAGCTTAGAGACAACATG	540						
QY	541	AGGTCCCGGTGTCTCAGACAATCTCTCCCAACAGCAGTGCCTCCAGAGCTACCAAGTG	600						
DB	541	AGGTCCCGGTGTCTCAGACAATCTCTCCCAACAGCAGTGCCTCCAGAGCTACCAAGTG	600						
QY	601	GCCACCTGATGCTCCACCGCAGCGGTAAAGACACCAAGTCCCGCGCGCATACGCA	660						
DB	601	GCCACCTGATGCTCCACCGCAGCGGTAAAGACACCAAGTCCCGCGCGCATACGCA	660						
QY	661	GCTCAGGGCTACAAAGTGTGGTGTCAACCCCTCGTTCGCTCAACAATGGCTTTGGT	720						
DB	661	GCTCAGGGCTACAAAGTGTGGTGTCAACCCCTCGTTCGCTCAACAATGGCTTTGGT	720						
QY	721	GCTTACATGTCCAAAGGCCAATGGATGATCTTAACATCAGAGCTGGGGTGAGGACAAT	780						
DB	721	GCTTACATGTCCAAAGGCCAATGGATGATCTTAACATCAGAGCTGGGGTGAGGACAAT	780						
QY	781	ACTACTGGACCGCGATCAGTATCCACTAGCGCAAGTTCCTTCCGACCGCGGTGT	840						
DB	781	ACTACTGGACCGCGATCAGTATCCACTAGCGCAAGTTCCTTCCGACCGCGGTGT	840						
QY	841	TCAGGGGTGCTTATGACATAATAATTTGTGACAGTGGCCACTCCACGGATGCAATCC	900						
DB	841	TCAGGGGTGCTTATGACATAATAATTTGTGACAGTGGCCACTCCACGGATGCAATCC	900						
QY	901	ATCTTGGGCAATGGCACTGCTTGAACAGACAGACCGCGGGCGGAGACTGCTGTG	960						
DB	901	ATCTTGGGCAATGGCACTGCTTGAACAGACAGACCGCGGGCGGAGACTGCTGTG	960						
QY	961	CTGCGCACCGCTACCCCTCGGGCTCCGTCACTGTGCCCACTCTTAACATCGAGGAGTT	1020						

DB	961	CTGCGCACCGCTACCCCTCGGGCTCCGTCACTGTGCCCACTCTTAACATCGAGGAGTT	1020						
QY	1021	GCTCTGTCCACTACCGAGAGATCCCTTTTATGGCAAGGCTATCCCTTTGAAGCAAT	1080						
DB	1021	GCTCTGTCCACTACCGAGAGATCCCTTTTATGGCAAGGCTATCCCTTTGAAGCAAT	1080						
QY	1081	AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAGAAGTGCAGAGCTCGCGCA	1140						
DB	1081	AAGGGGGGAGACATCTCATCTTCTGCCACTCAAGAGAAGTGCAGAGCTCGCGCA	1140						
QY	1141	AAACTCGTCCGCTGGCGCTCAATGCCGTGCTTACTACCGCGCTTATGTGTCCGTC	1200						
DB	1141	AAACTCGTCCGCTGGCGCTCAATGCCGTGCTTACTACCGCGCTTATGTGTCCGTC	1200						
QY	1201	ATCCCAACAGTGGTGAACCTTGTCTGCGGCAACTGACGCTCATGACCGCTTTTACC	1260						
DB	1201	ATCCCAACAGTGGTGAACCTTGTCTGCGGCAACTGACGCTCATGACCGCTTTTACC	1260						
QY	1261	GGGACTTCGANTCGGTGATAGACTGCAACAGTGTGTCAACAGACAGTCCAGCTTACG	1320						
DB	1261	GGGACTTCGANTCGGTGATAGACTGCAACAGTGTGTCAACAGACAGTCCAGCTTACG	1320						
QY	1321	CTTGACCTTACCTTCAACATTCAGACATCAAGCTTCCCGAGAGTCTGTCTCCGCTACT	1380						
DB	1321	CTTGACCTTACCTTCAACATTCAGACATCAAGCTTCCCGAGAGTCTGTCTCCGCTACT	1380						
QY	1381	CAACGTCCGGGTAGGACTGGCAGAGGGAAGCAGGATCTACAGATTTGTGGCACCAGGG	1440						
DB	1381	CAACGTCCGGGTAGGACTGGCAGAGGGAAGCAGGATCTACAGATTTGTGGCACCAGGG	1440						
QY	1441	GAGCGTCTTCTGGCATGTCTGACTCGTCTGCTCTGGAGTGTATGACCGGGTGT	1500						
DB	1441	GAGCGTCTTCTGGCATGTCTGACTCGTCTGCTCTGGAGTGTATGACCGGGTGT	1500						
QY	1501	GCTTGTGTAGACTTACGCCCCCGAGACCAAGTTAGGCTACGAGCATACATGAACACC	1560						
DB	1501	GCTTGTGTAGACTTACGCCCCCGAGACCAAGTTAGGCTACGAGCATACATGAACACC	1560						
QY	1561	CCGGACTTCCCGTGTGCCAGACCATCTTGAATTTTGGAGGGCGTCTTTACGGGTCTC	1620						
DB	1561	CCGGACTTCCCGTGTGCCAGACCATCTTGAATTTTGGAGGGCGTCTTTACGGGTCTC	1620						
QY	1621	ACCCACATAGACCGCCACTTCTATCCAGACAAAGCAGAGTGGGAAAACCTTCCCTAT	1680						
DB	1621	ACCCACATAGACCGCCACTTCTATCCAGACAAAGCAGAGTGGGAAAACCTTCCCTAT	1680						
QY	1681	CTGGTAGGTACCAAGCCACCGTGTGCGTAGAGCTCAAGCCCTTCCCGCGTCTGGGAC	1740						
DB	1681	CTGGTAGGTACCAAGCCACCGTGTGCGTAGAGCTCAAGCCCTTCCCGCGTCTGGGAC	1740						
QY	1741	CAGATGTGGAAGTGTCTGATCCGCTCAAGCCACCTTCCATGGCCCAACCTCTGCTA	1800						
DB	1741	CAGATGTGGAAGTGTCTGATCCGCTCAAGCCACCTTCCATGGCCCAACCTCTGCTA	1800						
QY	1801	TATAGACTGGGCGTGTCCAGATGAAGTCAACCTGACGACCCAGTCAACAGTATATC	1860						
DB	1801	TATAGACTGGGCGTGTCCAGATGAAGTCAACCTGACGACCCAGTCAACAGTATATC	1860						
QY	1861	ATGACATGTATGTGGCTGACCTGGAGTGTCTACAGATCACTGGGTCTCTGGTGGCGC	1920						
DB	1861	ATGACATGTATGTGGCTGACCTGGAGTGTCTACAGATCACTGGGTCTCTGGTGGCGC	1920						
QY	1921	GTTCGGCTGTCTTGGCGCGTATTCCTATCCACAGSCTCGTGTCTATAGTAGGTAGG	1980						
DB	1921	GTTCGGCTGTCTTGGCGCGTATTCCTATCCACAGSCTCGTGTCTATAGTAGGTAGG	1980						
QY	1981	ATTGTCTTGTCCGAAAGCCCGCAATCATACCCGACAGGGAAGTCTCTTACCGGAGTTC	2040						
DB	1981	ATTGTCTTGTCCGAAAGCCCGCAATCATACCCGACAGGGAAGTCTCTTACCGGAGTTC	2040						
QY	2041	GATGAAATGGAAGAGTGTCTGA	2061						

Db 2041 GATGAATGAAGAGTCTGA 2061

RESULT 3

HEC278830

LOCUS

DEFINITION

HEPATICITIS C VIRUS GENOMIC RNA FOR POLYPROTEIN GENE.

VERSION

HEC278830.1

KEYWORDS

GI:9843676

core protein; envelop protein 1; envelop protein 2; non-structural

protein 2; non-structural protein 3; non-structural protein 4a;

non-structural protein 4b; non-structural protein 5a;

non-structural protein 5b; ORF1; ORF10; ORF2; ORF3; ORF4; ORF5;

ORF6; ORF7; ORF8; ORF9; polyprotein.

Hepatitis C virus

Hepatitis C virus

viruses; serNA positive-strand viruses, no DNA stage; Flaviviridae;

Hepacivirus.

1

Kumar, U., Tuthill, T., Thomas, H. C. and Monjardino, J.

Sequence, expression and reconstitution of an HCV genome from a

British isolate derived from a single blood donation

J. Viral Hepat. 7 (6), 459-465. (2000)

21014672

11115058

REFERENCE

2 (bases 1 to 9610)

Kumar, U.

Direct Submission

Submitted (11-AUG-2000) Kumar U., Virology, GlaxoWellcome Research

centre, Gunneis Wood Road, Stevenage, Hertfordshire, SG1 2NY,

UNITED KINGDOM

LOCATION/Qualifiers

1. .9610

/organism="Hepatitis C virus"

/vixon

/mol_type="genomic RNA"

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/note="derived from serum of a non-A, non-B hepatitis

patient"

342. .9377

/note="unnamed protein product; ORF1"

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/db_xref="SPTREMBL:Q9DIT6"

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VGDLGCVFLVGLQFTSPRHWTTCQNCISYFGHITGRMDMMWMSPTALVY

AQLLRVPAIIDLTAHAGHWGLAIFYSMWNKAVLVVILLFAGVDANTYVITGGAA

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PCNIGVGNNTLHCPTDFRKHPEATYSCGSPWITPRCLVDYPRVWHYPCITLYN

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APILEVIGKGRHLLIFCHSKKCDLALAKVALGINAVAYRVDVSVITSGDVVVA

TDALMTGTFDGFSDICNTCTQTVDFSLDPTFTTETTLTPQDAVSRQRRGTGRG

KPGIVRFVAPGERFSGFDSAVLCECYDAGCAVELTPTAETTVRLRLVMTPLGVQC

HEC278830 9610 bp RNA linear VRL 03-JAN-2001
Hepatitis C virus genomic RNA for polyprotein gene.

AJ278830
HEC278830.1 GI:9843676
core protein; envelop protein 1; envelop protein 2; non-structural
protein 2; non-structural protein 3; non-structural protein 4a;
non-structural protein 4b; non-structural protein 5a;
non-structural protein 5b; ORF1; ORF10; ORF2; ORF3; ORF4; ORF5;
ORF6; ORF7; ORF8; ORF9; polyprotein.

Hepatitis C virus
Hepatitis C virus
viruses; serNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

1
Kumar, U., Tuthill, T., Thomas, H. C. and Monjardino, J.
Sequence, expression and reconstitution of an HCV genome from a
British isolate derived from a single blood donation
J. Viral Hepat. 7 (6), 459-465. (2000)

21014672
11115058
REFERENCE
2 (bases 1 to 9610)

Kumar, U.
Direct Submission
Submitted (11-AUG-2000) Kumar U., Virology, GlaxoWellcome Research
centre, Gunneis Wood Road, Stevenage, Hertfordshire, SG1 2NY,
UNITED KINGDOM

LOCATION/Qualifiers
1. .9610
/organism="Hepatitis C virus"
/vixon
/mol_type="genomic RNA"
/db_xref="taxon:11103"
/note="derived from serum of a non-A, non-B hepatitis
patient"
342. .9377
/note="unnamed protein product; ORF1"
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TILHSPGCPVPCVRGNSARCKVAVPTVATEDGKLPITLRRHIDLLVGSATLCSALY
VGDLGCVFLVGLQFTSPRHWTTCQNCISYFGHITGRMDMMWMSPTALVY
AQLLRVPAIIDLTAHAGHWGLAIFYSMWNKAVLVVILLFAGVDANTYVITGGAA
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PCNIGVGNNTLHCPTDFRKHPEATYSCGSPWITPRCLVDYPRVWHYPCITLYN
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ISOAPALENLVLNNAASLAGTRGLASFLVFFCPAWYLLKKGWFGRAIYLGWPLLL
LLIALLPQRAYALDTEMAASCGVVLVGLMALTLSPYKRYISWCFWMLQFLTRVFAH
LHWFPPLNVRGDAVILLVCVHTLFDITLKLALIFGLMILQTLKLLYVFAH
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PVWFQSMETKLTITGDDTAACDIIINGLPVARSRRREILGPDAGMVSKGRLAPIT
AVACOTRGLLCIIITSLTRDKNOVEGOVIOVTAOTFLATCINGCVTVYHGACTR
TIASPKGVPIQWYNVDOLWEPAPQASLPTCTCGSSDLVIVHEDVIVPVRERG
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GFQVMSKAGHDINIRGVTITGSPITYSTYKGLADGGCGGAYDIITICDECHS
TDATSLIGLTVLQCAETAGARLVLATATPPGVSVPVPHNIEVALSTGEIPFYKG
APILEVIGKGRHLLIFCHSKKCDLALAKVALGINAVAYRVDVSVITSGDVVVA
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CDS

DHLEFWEGVFTGLTHIDAHFLSQTQSGENLPLYVAYQATVCAQAQPPSPQWMMKC
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GLGKLVLDLAGYAGVAGALVAFKINGSPVSTEDKNLPAILPAGLAVGVVCAAT
LIRRHVGEGAGVQMMRLAFASRGHNVSPTHYVSPESDAARVAILLSLTVQLLR
RLHWVSESSTPPCSGWLADIDNMCIVLSDFKTLKAKLMFQPLQPLVLSVCOGRY
GWQGDGVMHTRCHGAEITGHVGNMTIRVGTCTKNMWSGTFPINAYTGPCTPLP
APNTYFALRVASAEYVIRRVDFHYVTGTTNLRCPQVSPSPFFTELDGVRLLR
FAPCKPLLRDEVSFRVGLHDYPVGSOLPCEPBDVAVTSLTDPDSHITABAGRLR
ARGSPSVASSASQLSAPSKAKCTTHDSDPAELTEANLLRWQMGNNITRVESN
KVVLDSPDPAVEDREVSVAELIKSRFAEALAIWARPDYNPPLLETWKKEDY
EPPVHSGCPFPPOSPPVPRKRTVTLTSTVSTALAEATKSGSSISGSGS
TTTSEPAPSVRSDEAESCSNPPLEGEPDLSGDSGSSVSSGADGEDVVCSSM
SYSWTGALVTPAAEBQKLPINALNSLLEHNLVSTTSRSACQKQKVTFORQLV
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LTCYKQAACRAAGLADCTMLVCCDDLVIYCISQGVQVEDAASLRAFTAMTRYVPP
RDPQPEYDLELITSCSNVSAVDHAGKXVYITLTDPTPLARAWEATARTPTPNSW
LGMTIMFAPTLWARMILMTHFFSVLMARDQEQALDEIYACYSIEPLDPIQRL
HGLSGLSHYSYSGEINRVAACLKGLVPLPRAWRHARSVRAKLLSRGAAICGKY
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915. .1490
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1491. .2768
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3420. .5312
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5313. .5474
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5475. .6257
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ORIGIN

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Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1519 CCCCGGAGACACAGTAGCTAGCAGGACATACATGACACCCCGGACTTCCCGTGC 1578
Db 4935 CCCCGGAGACACAGTAGCTAGCAGGACATACATGACACCCCGGACTTCCCGTGC 4994
QY 1579 CAAGACCATCTTGAATTTTGGAGGGCGTCTT 1610
Db 4995 CAAGACCATCTTGAATTTTGGAGGGCGTCTT 5026

RESULT 4

AF511949

LOCUS

9426 bp RNA linear VRL 13-JUN-2002

DEFINITION

Hepatitis C virus isolate XF223 polyprotein gene, complete

sequence.

ACCESSION AF511949
VERSION AF511949.1 GI:21397076
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 9426)
Hepatitis C virus
Fav, X. and Di Bisceglie, A.M.
TITLE Clonal Nature of Hepatitis C Virus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9426)
Fav, X. and Di Bisceglie, A.M.
AUTHORS Direct Submission
TITLE Submitted (14-MAY-2002) Gastroenterology & Hepatology, Saint Louis
JOURNAL University School of Medicine, 1402 South Grand Blvd., St. Louis,
MO 63104, USA
FEATURES
source Location/Qualifiers
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/organism="Hepatitis C virus"
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misc_feature 1..9426
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Best Local Similarity 100.0%; Pred. No. 4.6e-34;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1273 TCGGTGATAGACTGCAACACGTGTGTACCCAGACAGTCGACTTCAGCCCTTGACCCCTACC 1332
Db 4690 TCGGTGATAGACTGCAACACGTGTGTACCCAGACAGTCGACTTCAGCCCTTGACCCCTACC 4749
QY 1333 TTCACCATTCAGACAA 1348
Db 4750 TTCACCATTCAGACAA 4765
RESULT 5
A22779
LOCUS A22779 943 bp DNA linear PAT 24-JAN-1995
DEFINITION non-structural coding region.
ACCESSION A22779
VERSION A22779.1 GI:832940
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 943)
Hepatitis C virus
Fav, X. and Di Bisceglie, A.M.
TITLE Clonal Nature of Hepatitis C Virus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9426)
Fav, X. and Di Bisceglie, A.M.
AUTHORS Direct Submission
TITLE Submitted (14-MAY-2002) Gastroenterology & Hepatology, Saint Louis
JOURNAL University School of Medicine, 1402 South Grand Blvd., St. Louis,
MO 63104, USA
FEATURES
source Location/Qualifiers
1..943
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
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/isolate="XF223"
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/note="similar to polyprotein"
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Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1915 GCGCGGCTTCTGGCTGCTTTGGCGCGGTATTGCGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGGCTTCTGGCTGCTTTGGCGCGGTATTGCGCTATCCACAGGCTGCGTGCATAGTA 689
QY 1975 GG 1976

Db 690 GG 691
RESULT 6
AR031209
LOCUS AR031209 943 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 6 from patent US 5866139.
ACCESSION AR031209
VERSION AR031209.1 GI:5945498
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 943)
Brechot, C., Kreams, D. and Porchon, C.
AUTHORS Nucleotide and peptide sequences of a hepatitis C virus isolate,
TITLE diagnostic and therapeutic applications
JOURNAL Patent: US 5866139-A 6 02-FEB-1999;
FEATURES
source Location/Qualifiers
1..943
/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1915 GCGCGGCTTCTGGCTGCTTTGGCGCGGTATTGCGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGGCTTCTGGCTGCTTTGGCGCGGTATTGCGCTATCCACAGGCTGCGTGCATAGTA 689
QY 1975 GG 1976
Db 690 GG 691

Db 690 GG 691
RESULT 7
AR145025
LOCUS AR145025 943 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 6 from patent US 6210962.
ACCESSION AR145025
VERSION AR145025.1 GI:15106892
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 943)
Brechot, C., Kreams, D. and Porchon, C.
AUTHORS Nucleotide and peptide sequences of an isolate of the hepatitis C
TITLE virus, diagnostic and therapeutic applications thereof
JOURNAL Patent: US 6210962-A 6 03-APR-2001;
FEATURES
source Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 2e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1915 GCGCGGCTTCTGGCTGCTTTGGCGCGGTATTGCGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGGCTTCTGGCTGCTTTGGCGCGGTATTGCGCTATCCACAGGCTGCGTGCATAGTA 689
QY 1975 GG 1976
Db 690 GG 691

HPCNS3NS4
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

HPCNS3NS4
 Hepatitis C virus NS3/NS4 gene for ORF 1, partial cds.
 D10664 D01103
 D10664.1 GI:221623
 nonstructural protein; NS3/NS4.
 Hepatitis C virus
 Hepatitis C virus
 Viruses; sRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

1 (bases 1 to 943)
 Krensdorf, D., Porchon, C., Kim, J.P., Reyes, G.R. and Brechot, C.
 Partial nucleotide sequence analysis of a French hepatitis C virus:
 implications for HCV genetic variability in the E2/NS1 protein
 J. Gen. Virol. 72 (Pt 10), 2557-2561 (1991)
 92013977
 1655961
 2 (sites)
 Mink, M.A., Benichou, S., Madaule, P., Tiollais, P., Prince, A.M. and
 Inchausti, G.
 Characterization and mapping of a B-cell immunogenic domain in
 hepatitis C virus E2 glycoprotein using a yeast peptide library
 Virology 200 (1), 246-255 (1994)
 94174722
 7510436
 3 (bases 1 to 943)
 Krensdorf, D.
 Direct Submission
 Submitted (17-JUL-1991) Dina Krensdorf, INSERM U75; CHU Necker,
 156, rue de Vaugirard, Paris 75015, France (E-mail:BEAUNE@PRC1T151,
 Tel:40659911)

FEATURES
 source

1..943
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 /db_xref="taxon:11103"
 /note="isolated from serum of human patient MIC"
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gene
 CDS

ORIGIN

Query Match 3.0%; Score 62; DB 14; Length 943;
 Best Local Similarity 100.0%; Pred. No. 2e-25;
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1915 GCGCGCGTTCGGCTGCTTTGCCCGCGATTGCCCTATCCACAGCGTGGTGCATAGTA 1974
 Db 630 GCGCGCGTTCGGCTGCTTTGCCCGCGATTGCCCTATCCACAGCGTGGTGCATAGTA 689
 Qy 1975 GG 1976
 Db 690 GG 691

RESULT 9
 AF290978
 LOCUS
 DEFINITION
 ACCESSION
 VERSION

AF290978
 Hepatitis C virus isolate colone1 complete genome.
 AF290978.1 GI:9930556

INSVWKDLSDSVTPIDTTIWAKEVFCVOPKGGKPKPARLIVPPDLGVRVCEKMAIY
DVVSKLPVAVGSSVGFQYSGQVFEVLVQWKKTPMGFSYDTRCFDSVYESDIR
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GDPQPEYDELITSCSNVSVADHGAGKRVYILTRDFTPLARAWEATHTPTVNSW
LGNIMFAPLETWARMILMTHFFSVLIARDQFEQALNCEIYGCACVSIPLDLPPIQRL
HGLSFAHSYSGEINRVAACLRKIGVPLRAWKHRARSVRARLLSRGGRAALCGKY
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VGIYLLPNR"

ORIGIN
Query Match 3.0%; Score 62; DB 14; Length 9365;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 GCTACCCCTCCGGCTCGTCACTGTGCCCCCATCTTAACATCGAGAGGTTGCTCTGCC 1029
D 4374 GCTACCCCTCCGGCTCGTCACTGTGCCCCCATCTTAACATCGAGAGGTTGCTCTGCC 4433
QY 1030 AC 1031
D 4434 AC 4435

RESULT 10
AF511950 9395 bp RNA linear VRL 13-JUN-2002
LOCUS Hepatitis C virus isolate XF224 polyprotein gene, complete
DEFINITION
ACCESSION AF511950
VERSION AF511950.1 GI:21397077
KEYWORDS
SOURCE
ORGANISM Hepatitis C virus
Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus

REFERENCE 1 (bases 1 to 9395)
AUTHORS Fan, X. and Di Bisceglie, A.M.
TITLE Clonal Nature of Hepatitis C Virus
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 9395)
AUTHORS Fan, X. and Di Bisceglie, A.M.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2002) Gastroenterology & Hepatology, Saint Louis University School of Medicine, 1402 South Grand Blvd., St. Louis, MO 63104, USA

FEATURES
source
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/organism="Hepatitis C virus"
/mol_type="genomic RNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY -970 GCTACCCCTCCGGCTCGTCACTGTGCCCCCATCTTAACATCGAGAGGTTGCTCTGCC 1029
D 4358 GCTACCCCTCCGGCTCGTCACTGTGCCCCCATCTTAACATCGAGAGGTTGCTCTGCC 4417
QY 1030 AC 1031
D 4418 AC 4419

RESULT 11
BD226202 957 bp DNA linear PAT 17-JUL-2003
LOCUS

DEFINITION Improved immunodiagnostic assays using reducing agents.
ACCESSION BD226202
VERSION BD226202.1 GI:33035972
KEYWORDS JP 2002512370-A/4.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE 1 (bases 1 to 957)
AUTHORS Maertens, G., Louwagie, J., Bosman, A., Sablon, E. and Zreïn, M.
TITLE Improved immunodiagnostic assays using reducing agents
JOURNAL Patent: JP 2002512370-A 4 23-APR-2002;
INNOGENETICS NV

COMMENT OS Hepatitis virus (hepatitis C virus)
PN JP 2002512370-A/4
ED 23-APR-2002
PF 15-APR-1999 JP 2000545027
PR 17-APR-1998 EP 98870087.8
PI GEERT MAERTENS, JOOST LOUWAGIE, ALFONS BOSMAN, ERWIN SABLON, MAAN ZREIN
PC G01N33/543, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/00 PC
C12N15/09, C12Q1/25,
PC C12Q1/68, G01N33/573, G01N33/576, C12N5/00, C12N15/00 CC
Improved immunodiagnostic assays using reducing agents FH Key
Location/Qualifiers
FT source 1. .957
virus), /organism="Hepatitis virus (hepatitis C FT

FEATURES
source
1. .957 Location/Qualifiers
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 3.0%; Score 61; DB 6; Length 957;
Best Local Similarity 100.0%; Pred. No. 8.5e-25;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 710 TGGGTTTGCTGCTTACATGTCACAGGCCATCGGATTCATCTAACATCAGGACTGGG 769
D 344 TGGGTTTGCTGCTTACATGTCACAGGCCATCGGATTCATCTAACATCAGGACTGGG 403
QY 770 T 770
D 404 T 404

RESULT 12
HPCNS10CLN 241 bp ss-RNA linear VRL 02-AUG-1993
LOCUS Hepatitis C virus (clone #10) nonstructural protein (NS3/NS4) gene, partial cds.
DEFINITION
ACCESSION M94401 M84480
VERSION M94401.1 GI:329772
KEYWORDS nonstructural protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1 (bases 1 to 241)
AUTHORS Martell, M., Esteban, J.I., Quer, J., Genesca, J., Weiner, A., Esteban, R., Guardia, J. and Gomez, J.
TITLE Hepatitis C virus (HCV) circulates as a population of different but closely related genomes: quasispecies nature of HCV genome distribution
JOURNAL J. Virol. 66 (5), 3225-3229 (1992)
MEDLINE 92219420
PubMed 1313927

COMMENT Original source text: Hepatitis C virus RNA.
FEATURES
1. .241 Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic RNA"

gene /db_xref="taxon:11103"
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 /gene="NS3/NS4"
 CDS <1. .>241
 /gene="NS3/NS4"
 /codon_start=2
 /product="nonstructural protein"
 /protein_id="AAA45608.1"
 /db_xref="GI:329773"
 /translation="LRAVMNTPGLPVCCDHLFEWGVFTGLTHDAHFLSQTQSGEN
 LFLVAYQATVCARAQAPPPSDQWQWKLRLKPTL"

ORIGIN

Query Match 2.9%; Score 59; DB 14; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.4e-23;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 TACATGAACACCCCGGACTTCCCGTGTGCCAAGACCATCTTGATTTGGAGGGCGT 1607
 Db 11 TACATGAACACCCCGGACTTCCCGTGTGCCAAGACCATCTTGATTTGGAGGGCGT 69

RESULT 13

HPCNS11CLN 241 bp ss-RNA linear VRL 02-AUG-1993
 LOCUS Hepatitis C virus (clone #11) nonstructural protein (NS3/NS4) gene,
 DEFINITION partial cds.
 ACCESSION M94400.1 GI:329774
 VERSION nonstructural protein.
 KEYWORDS Hepatitis C virus
 SOURCE Hepatitis C virus
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Hepacivirus.

REFERENCE

1. (bases 1 to 241)
 Martell,M., Esceban,J.I., Quer,J., Genesca,J., Weiner,A.,
 Esteban,R., Guardia,J. and Gomez,J.
 Hepatitis C virus (HCV) circulates as a population of different but
 closely related genomes: quasiespecies nature of HCV genome
 distribution
 J. Virol. 66 (5), 3225-3229 (1992)

JOURNAL

92219420
 MEDLINE

1313927
 PUBMED

COMMENT Original source text: Hepatitis C virus RNA.

FEATURES

source Location/Qualifiers
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 /organism="Hepatitis C virus"
 /mol_type="genomic RNA"
 /db_xref="taxon:11103"
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 /codon_start=2
 /product="nonstructural protein"
 /protein_id="AAA45609.1"
 /db_xref="GI:329775"
 /translation="LRAVMNTPGLPVCCDHLFEWGVFTGLTHDAHFLSQTQSGEN
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gene

CDS

ORIGIN

Query Match 2.9%; Score 59; DB 14; Length 241;
 Best Local Similarity 100.0%; Pred. No. 1.4e-23;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1549 TACATGAACACCCCGGACTTCCCGTGTGCCAAGACCATCTTGATTTGGAGGGCGT 1607
 Db 11 TACATGAACACCCCGGACTTCCCGTGTGCCAAGACCATCTTGATTTGGAGGGCGT 69

RESULT 14

HCVNSTP 550 bp RNA linear VRL 27-APR-1994
 LOCUS

DEFINITION Hepatitis C Virus sequence for non-structural protein.
 ACCESSION X71406
 VERSION 1 GI:296161
 KEYWORDS hepatitis; non-structural protein; NS3/NS4.
 SOURCE Hepatitis C virus
 ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 Hepacivirus.

REFERENCE

1. Vassilev,V.B., Viazov,S.O., Kotova,E.Y. and Nosikov,V.V.
 Determination of the nucleotide sequence of the Russian variant of
 the hepatitis C virus
 Mol. Gen. Mikrobiol. Virusol. 1, 33-37 (1994)

JOURNAL

2 (bases 1 to 550)
 Vassilev,V.B.

AUTHORS

TITLE

JOURNAL

Submitted (13-APR-1993) V.B. Vassilev, Institute of Genetics &
 Selection of Industrial Microorganisms, 1-st Dorozhny proezd str.,
 1, 113545 Moscow, Russia, USSR

FEATURES

source Location/Qualifiers
 1. .550
 /organism="Hepatitis C virus"
 /mol_type="genomic RNA"
 /variety="Russian isolate"
 /isolate="patient 11, with chronic non-A, non-B
 post-transfusion hepatitis"
 /db_xref="taxon:11103"
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 /gene="NS3 /NS4"
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 /gene="NS3 /NS4"
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 /protein_id="C3850530.1"
 /db_xref="GI:296162"
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 /db_xref="GOA:Q68960"
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 GERPSGMFSDSVLCEYDAGCAWELTPTAETVRLRAYMNTPLPVCCDHLFEWGVFT
 TGLTQIDAHLFSOTKSGENLPLVAYQATVCARAQAPPPSDQWQWKLRLKPTLHG
 PTPLLVRLGAVQNEVTLTHPVT"

gene

CDS

ORIGIN

Query Match 2.9%; Score 59; DB 14; Length 550;
 Best Local Similarity 100.0%; Pred. No. 1.5e-23;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1567 CTTCCTGGTGCCCAAGACCATCTTGATTTGGAGGGCGTCTTTACGGTCTCACCCA 1625
 Db 264 CTTCCTGGTGCCCAAGACCATCTTGATTTGGAGGGCGTCTTTACGGTCTCACCCA 322

RESULT 15

LOCUS

HPCNS34
 Hepatitis C virus nonstructural region.

DEFINITION

Accession M60220

VERSION

M60220.1 GI:329802
 nonstructural region.

KEYWORDS

SOURCE

Hepatitis C virus
 Hepacivirus.

REFERENCE

1 (bases 1 to 1477)
 Li,J.S., Tong,S.P., Vitvitski,L., Lepot,D. and Trepo,C.

AUTHORS

TITLE

Two French genotypes of hepatitis C virus: homology of the
 predominant genotype with the prototype American strain

JOURNAL

Gene 105 (2), 167-172 (1991)

MEDLINE

92039028
 PUBMED

COMMENT

Original source text: Hepatitis C virus (strain Fla) plasma DNA.
 Location/Qualifiers
 1. .1477

/organism="Hepatitis C virus"
 /mol_type="genomic DNA"
 /strain="Fla"
 /db_xref="taxon:11103"
 /tissue_type="plasma"

ORIGIN
 Query Match 2.8%; Score 59; DB 14; Length 1477;
 Best Local Similarity 100.0%; Pred. No. 1.5e-23;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1903 TGGGTGCTCGTTGGCGCGGTTCTGGCTGCTTTGGCCGCGTATTGCCATTCCACAGGCTG 1961
 |||
 DB 632 TGGGTGCTCGTTGGCGCGGTTCTGGCTGCTTTGGCCGCGTATTGCCATTCCACAGGCTG 690
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RESULT 16
 AR124773 382 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 56 from patent US 6172189.
 AR124773
 VERSION AR124773.1 GI:14110134
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 382)
 AUTHORS Devare,S.G., Desai,S.M., Casey,J.M., Dailey,S.H., Dawson,G.J.,
 Gutierrez,R.A., Lesniowski,R.R., Stewart,J.L. and Rupprecht,K.R.
 TITLE Hepatitis C assay utilizing recombinant antigens
 JOURNAL Patent: US 6172189-A 56 09-JAN-2001;
 FEATURES Location/Qualifiers
 source 1..382
 /organism="unknown"
 /mol_type="unassigned DNA"

ORIGIN
 Query Match 2.8%; Score 58; DB 6; Length 382;
 Best Local Similarity 100.0%; Pred. No. 6e-23;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACCTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCCCTACCTTCACCATTTGAGCAA 1348
 |||
 DB 33 ACCTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCCCTACCTTCACCATTTGAGCAA 90
 |||

RESULT 17
 AR353560 382 bp DNA linear PAT 17-AUG-2003
 LOCUS
 DEFINITION Sequence 56 from patent US 6593083.
 AR353560
 ACCESSION AR353560.1 GI:33759550
 VERSION
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 382)
 AUTHORS Devare,S.G., Desai,S.M., Casey,J.M., Dailey,S.H., Dawson,G.J.,
 Gutierrez,R.A., Lesniowski,R.R., Stewart,J.L. and Rupprecht,K.R.
 TITLE Hepatitis C assay utilizing recombinant antigens
 JOURNAL Patent: US 6593083-A 56 15-JUL-2003;
 FEATURES Location/Qualifiers
 source 1..382
 /organism="unknown"
 /mol_type="genomic DNA"

ORIGIN
 Query Match 2.8%; Score 58; DB 6; Length 382;
 Best Local Similarity 100.0%; Pred. No. 6e-23;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACCTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCCCTACCTTCACCATTTGAGCAA 1348
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REFERENCE 1 (bases 1 to 1420)
AUTHORS Devare,S.G., Desai,S.M., Casey,J.M., Dailey,S.H., Dawson,G.J.,
Gutierrez,R.A., Lesniewski,R.R., Stewart,J.L. and Rupprecht,K.R.
TITLE Hepatitis C assay utilizing recombinant antigens
JOURNAL Patent: US 6172189-A 57 09-JAN-2001;
FEATURES
source
1. .1420
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.8%; Score 58; DB 6; Length 1420;
Best Local Similarity 100.0%; Pred. No. 6.1e-23;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACGTGTGTACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGCAA 1348
DB 22 ACGTGTGTACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGCAA 79

RESULT 21
LOCUS AR353561 1420 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 57 from patent US 6593083
ACCESSION AR353561
VERSION AR353561.1 GI:33759551
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1420)
AUTHORS Devare,S.G., Desai,S.M., Casey,J.M., Dailey,S.H., Dawson,G.J.,
Gutierrez,R.A., Lesniewski,R.R., Stewart,J.L. and Rupprecht,K.R.
TITLE Hepatitis C assay utilizing recombinant antigens
JOURNAL Patent: US 6593083-A 57 15-JUL-2003;
FEATURES
source
1. .1420
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 2.8%; Score 58; DB 6; Length 1420;
Best Local Similarity 100.0%; Pred. No. 6.1e-23;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACGTGTGTACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGCAA 1348
DB 22 ACGTGTGTACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGCAA 79

RESULT 22
LOCUS HPCHCV35 162 bp ss-RNA linear VRL 20-MAY-1994
DEFINITION Hepatitis C virus mRNA, partial cds.
ACCESSION M55151
VERSION M55151.1 GI:329764
KEYWORDS
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 162)
AUTHORS Ulrich,P.P., Romeo,J.M., Lane,P.K., Kelly,I., Daniel,L.J. and
Vyas,G.N.
TITLE Detection, semiquantitation, and genetic variation in hepatitis C
virus sequences amplified from the plasma of blood donors with
elevated alanine aminotransferase
J. Clin. Invest. 86 (5), 1609-1614 (1990)
91056164
2173725
ORIGINAL SOURCE text: Hepatitis C virus, cDNA to genomic RNA, from
human plasma.
Location/Qualifiers

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1. .162
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/map="2895-3056"
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/organism="HCV"
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/feature="ORF"
/codon_start=1
/protein_id="AAA45605.1"
/db_xref="GI:329765"
/translation="VAYYRGLDVSVIPTSGDVVVVATDALMTGYTGDFDSVIDCNTCV
TQVDFSLDP"

ORIGIN
Query Match 2.8%; Score 57; DB 14; Length 162;
Best Local Similarity 100.0%; Pred. No. 2.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1273 TCGGTGATAGACTGCAACACGCTGTGTACCCAGACAGTCGACTTCAGCCTTGACCTT 1329
DB 106 TCGGTGATAGACTGCAACACGCTGTGTACCCAGACAGTCGACTTCAGCCTTGACCTT 162

RESULT 23
LOCUS HPNS17CLN 223 bp ss-RNA linear VRL 02-AUG-1993
DEFINITION Hepatitis C virus (clone #17) nonstructural protein (NS3/NS4) gene,
partial cds.
ACCESSION M94451 M84480
VERSION M94451.1 GI:329778
KEYWORDS nonstructural protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE 1 (bases 1 to 223)
AUTHORS Martell,M., Esteban,J.I., Quer,J., Genesca,J., Weiner,A.,
Esteban,R., Guardia,J. and Gomez,J.
TITLE Hepatitis C virus (HCV) circulates as a population of different but
closely related genomes: Quasispecies nature of HCV genome
distribution
J. Virol. 66 (5), 3225-3229 (1992)
92219420
1313927
COMMENT Original source text: Hepatitis C virus RNA.
FEATURES
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Location/Qualifiers
/organism="Hepatitis C virus"
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/product="nonstructural protein"
/protein_id="AAA45611.1"
/db_xref="GI:329779"
/translation="TPGLPVQCVHLEFWGVFTGITHDAHFLSKQSGENLPYLVA
YQATVCARAQAAPPSPWDQMKLRLKPTL"

ORIGIN
Query Match 2.8%; Score 57; DB 14; Length 223;
Best Local Similarity 100.0%; Pred. No. 2.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1723 CCTCCCCCGTCGTGGAGCAGATGCGAGTCTTGATCGTTCAGGCCACCCCTC 1779
DB 167 CCTCCCCCGTCGTGGAGCAGATGCGAGTCTTGATCGTTCAGGCCACCCCTC 228

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RESULT 24
LOCUS HPCNS15CLN 229 bp ss-RNA linear VRL 02-AUG-1993
DEFINITION Hepatitis C virus (clone #15) nonstructural protein (NS3/NS4) gene,
partial cds.
ACCESSION M94449 M84480
VERSION M94449.1 GI:329776
KEYWORDS nonstructural protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 229)
AUTHORS Martell,M., Esteban,J.I., Quer,J., Genesca,J., Weiner,A.,
Esteban,R., Guardia,J. and Gomez,J.
TITLE Hepatitis C virus (HCV) circulates as a population of different but
closely related genomes: quasisppecies nature of HCV genome
distribution
J. Virol. 66 (5), 3225-3229 (1992)
MEDLINE 92219420
PUBMED 1313927
COMMENT Original source text: Hepatitis C virus RNA.
FEATURES
source
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Location/Qualifiers
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/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/db_xref="taxon:11103"
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/product="nonstructural protein"
/db_xref="GI:329776"
/translaton="MNTPLPVCODHLEFWEVFTGLTHIDAFSLQTKQSGNLFYL
VAYQATVCARAQAAPPSPWDQWKILRLKPTL"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1551 CATGAACACCCCGGACTTCCCGTGCAGACCATCTTGAATTTGGAGGCGT 1607
|||||
Db 1 CATGAACACCCCGGACTTCCCGTGCAGACCATCTTGAATTTGGAGGCGT 57
|||||

RESULT 25
LOCUS HPCNSCLN5 241 bp ss-RNA linear VRL 02-AUG-1993
DEFINITION Hepatitis C virus (clone #5) nonstructural protein (NS3/NS4) gene,
partial cds.
ACCESSION M94469 M84480
VERSION M94469.1 GI:329852
KEYWORDS nonstructural protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.
REFERENCE 1 (bases 1 to 241)
AUTHORS Martell,M., Esteban,J.I., Quer,J., Genesca,J., Weiner,A.,
Esteban,R., Guardia,J. and Gomez,J.
TITLE Hepatitis C virus (HCV) circulates as a population of different but
closely related genomes: quasisppecies nature of HCV genome
distribution
J. Virol. 66 (5), 3225-3229 (1992)
MEDLINE 92219420
PUBMED 1313927
COMMENT Original source text: Hepatitis C virus RNA.
FEATURES
source
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Location/Qualifiers
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/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/db_xref="taxon:11103"
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/product="nonstructural protein"
/db_xref="GI:329852"
/translaton="MNTPLPVCODHLEFWEVFTGLTHIDAFSLQTKQSGNLFYL
VAYQATVCARAQAAPPSPWDQWKILRLKPTL"

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/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/db_xref="taxon:11103"
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/gene="NS3/NS4"
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/product="nonstructural protein"
/protein_id="AAA45675.1"
/db_xref="GI:329853"
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LFYVAYQATVCARAQAAPPSPWDQWKILRLKPTL"
ORIGIN
Query Match 2.8%; Score 57; DB 14; Length 241;
Best Local Similarity 100.0%; Pred. No. 2.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1723 CTTCCCTCGTGGGACGAGATGCGAGTCTTGTATCCGTCCTCAAGCCACCTC 1779
|||||
Db 185 CTTCCCTCGTGGGACGAGATGCGAGTCTTGTATCCGTCCTCAAGCCACCTC 241
|||||

RESULT 26
LOCUS I32190 281 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 75 from patent US 5585258.
ACCESSION I32190
VERSION I32190.1 GI:1822981
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 281)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5585258-A 75 17-DEC-1996;
FEATURES
source
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/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGTGCAGGCGACGCGGATGTATCC 347
|||||
Db 4 TGCACCTTGGGCTCTCGGACCTTTACCTGTGCAGGCGACGCGGATGTATCC 59
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RESULT 27
LOCUS I34281 281 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 75 from patent US 5597691..
ACCESSION I34281
VERSION I34281.1 GI:1825072
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 281)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5597691-A 75 28-JAN-1997;
FEATURES
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/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

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REXX

REXX

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Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 347
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Db 4 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 59

RESULT 28
LOCUS I82486 281 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 75 from patent US 5712145.
ACCESSION I82486
VERSION I82486.1 GI:3210783
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 281)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5712145-A 75 27-JAN-1998;
FEATURES
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source /organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match      2.7%; Score 56; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 347
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Db 4 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 59

RESULT 29
LOCUS BD140411 281 bp DNA linear PAT 18-SEP-2002
DEFINITION Hepatitis C virus protease.
ACCESSION BD140411
VERSION BD140411.1 GI:23235356
KEYWORDS JP 2002051791-A/29.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
REFERENCE
1 (bases 1 to 281)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: JP 2002051791-A 29 19-FEB-2002;
COMMENT CHIRON CORP
OS HCV
PN JP 2002051791-A/29
PD 19-FEB-2002
PR 11-JUN-2001 JP 2001176369
PP 04-APR-1990 US 505433
PI MICHAEL HOUGHTON,QUI LIM CHOO,GEORGE KUO
PC C12N15/09,C12N15/09,C12N9/50/(C12N9/50,C12R1:93),(C12N15/09,
PC C12R1:93),C12N15/00,C12N15/00,C12R1:93)
PC C12N15/00,C12N15/00,C12N15/00,C12R1:93)
CC Hepatitis C virus protease
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
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source /organism="Hepatitis C virus"
/mol_type="genomic DNA"
/db_xref="taxon:11103"
ORIGIN

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Query Match      2.7%; Score 56; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 347
    |||
Db 4 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 59

RESULT 30
LOCUS AR118676 283 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 33 from patent US 6150087.
ACCESSION AR118676
VERSION AR118676.1 GI:14100586
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 283)
AUTHORS Chien,D.Y.
TITLE NANBV diagnostics and vaccines
JOURNAL Patent: US 6150087-A 33 21-NOV-2000;
FEATURES
1..283
source /organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match      2.7%; Score 56; DB 6; Length 283;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 347
    |||
Db 6 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 61

RESULT 31
LOCUS I32188 368 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 71 from patent US 5585258.
ACCESSION I32188
VERSION I32188.1 GI:1822979
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 368)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5585258-A 71 17-DEC-1996;
FEATURES
1..368
source /organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match      2.7%; Score 56; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 347
    |||
Db 220 TGCACCTTGGCGGCTCCTCGGACCTTTACTGTCACGAGGCACGCCGATGTCATTC 275

RESULT 32
LOCUS I34279 368 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 71 from patent US 5597691.
ACCESSION I34279
VERSION I34279.1 GI:1825070

```

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	Houghton, M., Choo, Q.-L. and Kuo, G.
TITLE	Hepatitis C virus protease
JOURNAL	Patent: US 5597691-A 71 28-JAN-1997;
FEATURES	Location/Qualifiers
source	1..368
ORIGIN	/organism="unknown"
Query Match	2.7%; Score 56; DB 6; Length 368;
Best Local Similarity	100.0%; Pred. No. 1e-21;
Matches	56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	292 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTACAGGAGCGACGCGGATGTCATTCC 347
Db	220 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTACAGGAGCGACGCGGATGTCATTCC 275
RESULT 33	
LOCUS	182484 368 bp DNA linear PAT 10-JUN-1998
DEFINITION	Sequence 71 from patent US 5712145.
ACCESSION	182484
VERSION	182484.1 GI:3210781
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	1 (bases 1 to 368)
AUTHORS	Houghton, M., Choo, Q.-L. and Kuo, G.
TITLE	Hepatitis C virus protease
JOURNAL	Patent: US 5712145-A 71 27-JAN-1998;
FEATURES	Location/Qualifiers
source	1..368
ORIGIN	/organism="unknown"
Query Match	2.7%; Score 56; DB 6; Length 368;
Best Local Similarity	100.0%; Pred. No. 1e-21;
Matches	56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	292 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTACAGGAGCGACGCGGATGTCATTCC 347
Db	220 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTACAGGAGCGACGCGGATGTCATTCC 275
RESULT 34	
LOCUS	BD140409 368 bp DNA linear PAT 18-SEP-2002
DEFINITION	Hepatitis C virus protease.
ACCESSION	BD140409
VERSION	BD140409.1 GI:23235354
KEYWORDS	JP 2002051791-A/27.
SOURCE	Hepatitis C virus
ORGANISM	Hepatitis C virus
REFERENCE	1 (bases 1 to 368)
AUTHORS	Houghton, M., Choo, Q.-L. and Kuo, G.
TITLE	Hepatitis C virus protease
JOURNAL	Patent: JP 2002051791-A 27 19-FEB-2002;
COMMENT	CHIRON CORP
OS	HCV
PN	JP 2002051791-A/27
PD	19-FEB-2002
PF	11-JUN-2001 JP 2001176369
PR	04-APR-1990 US 505433

Db 289 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATCC 344

RESULT 36
LOCUS HPCNS3PROB 1284 bp ss-RNA linear VRL 10-JUN-1996
DEFINITION Hepatitis C virus nonstructural (NS3) gene 5', 5' end.
ACCESSION M62386
VERSION M62386.1 GI:329832
KEYWORDS nonstructural protein.
SOURCE Hepatitis C virus
ORGANISM Hepatitis C virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Hepacivirus.
REFERENCE 1 (bases 1 to 1284)
Ogata,N., Alter,H.J., Miller,R.H. and Purcell,R.H.
Nucleotide sequence and mutation rate of the H strain of hepatitis C virus
Proc. Natl. Acad. Sci. U.S.A. 88 (8), 3392-3396 (1991)
JOURNAL 91195357
MEDLINE 1849654
COMMENT Original source text: Hepatitis C virus RNA.
FEATURES
Location/Qualifiers
1..1284
/organism="Hepatitis C virus"
/mol_type="genomic RNA"
/specific host="Patient H 1990"
/db_xref="taxon:11103"
1..1284
/gene="NS3"
<1..>1284
/gene="NS3"
/codon_start=1
/product="polyprotein"
/protein_id="AAB02125.1"
/db_xref="GI:1303664"
/translation="VFQDMSPPAVPQSFQVAHLHPTGSGKSTKVPYAAVAGQYKVL
VLNPSVAATGFGYMSKAYGIDPSIKTGRTITIGSPITYSTYIGKFLADGGSGGAY
DIIICDECHSTDATSLIGLIDQAEAGARLVLAATAPPGSVTVSPHNIEEVALS
TTGIRPYGKAIPLGVTKGRHLIFCHSKKKDELAALVALGVNAVAYRGLDVSVI
PTSGDVVVSTDALMTGTGDFSDVIDNCVTQVDFSLDPTFTIETTLPLQDAVSR
TORGRGRGKPGIYRFVAPGERSGMFDSVLCECVACGAWELTPTAETTVRLRAY
KNTPLGVCDHLEFMEGVTGLTHDAHFLSQKSGENFPYLVAYQATVCARAQAP
PFSWDQWKKLIRUKPLRHGTPLRLYLGLAVQNEVI"
1..>1284
mat_peptide
/gene="NS3"
/product="nonstructural protein"

ORIGIN
Query Match 2.7%; Score 56; DB 14; Length 1284;
Best Local Similarity 100.0%; Pred. No. 1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 GTGGCCCACTTGCATGCTCCACCGGACGGTAAAGACCAAGGTCCTCCGGCGC 653
DB 49 GTGGCCCACTTGCATGCTCCACCGGACGGTAAAGACCAAGGTCCTCCGGCGC 104

RESULT 37
LOCUS AR404933 2058 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 2 from patent US 6630298.
ACCESSION AR404933
VERSION AR404933.1 GI:40153764
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2058)
Chien,D.Y., Arcangel,P., Tandeske,L., George-Nascimento,C., Coit,D.
and Medina-Selby,A.
HCV antigen/antibody combination assay
Patent: US 6630298-A 2 07-OCT-2003;
JOURNAL

FEATURES
Location/Qualifiers
1..2058
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATCC 347
DB 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATCC 347

RESULT 38
LOCUS AR408362 2058 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6632601.
ACCESSION AR408362
VERSION AR408362.1 GI:40158513
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2058)
Chien,D.Y., Arcangel,P., Tandeske,L., George-Nascimento,C., Coit,D.
and Medina-Selby,A.
Immunosays for anti-HCV antibodies
Patent: US 6632601-A 1 14-OCT-2003;
JOURNAL
FEATURES
Location/Qualifiers
1..2058
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATCC 347
DB 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATCC 347

RESULT 39
LOCUS AX395309 2058 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 2 from Patent WO0196875.
ACCESSION AX395309
VERSION AX395309.1 GI:21066308
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
Chien,D.Y., Arcangel,P., Tandeske,L., George-Nascimento,C.,
Coit,D. and Medina-Selby,A.
Hcv antigen/antibody combination assay
Patent: WO 0196875-A 2 20-DEC-2001;
JOURNAL CHIRON CORPORATION (US)
FEATURES
Location/Qualifiers
1..2058
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="representative NS3/4a conformational antigen"
1..>2058
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAD32154.1"
/db_xref="GI:21066309"

CDS

/db_xref="RENTREMBL:CAD32154"
/translation="MAPITAYAOOTRGILGLILITSLTRDKNOVEGEVOIVSTAQTF
LATCINGVCTVHVGACRTIAEPKGVIOYNTVDQDLVGNWPAQSGSLPCTCGS
SDLYLVTRHADVIPIRRGDSRGLSPREISYLNKSGGGLPCPAGHVGIVFRAVC
TRGAKAVDFIPVENLETTMRSPVFTDINSPPVPPQSFQVAHLHPTGSGSKTKVPA
YAAQGYKVLNLSVAATLFGAYMSKAHGINENRTGRTVITITGSPITYSTYKFLA
DGGSGGAYDIIICDECHSDATSLIGITVLDQETAGARLVLAATATPPGVTVP
PNIIEVALSTGTEIPFYKAIPLKVIKGRHLFCHSKKCDLAAKLVALGINAVAY
YRGDLVSVIPPIGDVVVATDALMTGVTGDFDSVIDCNTCTVTQVDPGLDPTFTETI
TLPODAVSRTOGRGTRGKGLYRFVARGERSGMDSSVLCQDAGCAYELVTPA
ETTVRLAYNTPGLPCQDHLFEWEGVTGLTHIDAHFLSQTKQSGENPLVAYQ
TVCARAQAPPSDQMKCLIRKLPILHGTPLLYRLGAVONEITLTHPVTKYIMTCM
SADLEVVSTWLVVGGVLAALAYCLSTGCVIIVGRVLSGRPAIIPDREVLYRFEDE
MEEC"

ORIGIN

Query Match 2.7%; Score 56; DB 6; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 347
Db 292 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 347

RESULT 40

AX454818
LOCUS 2058 bp DNA linear PAT 06-JUL-2002
DEFINITION Sequence 1 from Patent WO0196870.
ACCESSION AX454818
VERSION AX454818.1 GI:21714047

KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.

REFERENCE

1 Chien,D.Y., Arcangel,P., Tandeske,L., George-Nascimento,C.,
Cicit,D. and Medina-Seiby,A.
Immunassays for anti-hcv antibodies
Patent: WO 0196870-A 1 20-DEC-2001;
CHIRON CORPORATION (US)

FEATURES

1..2058
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="representative NS3/4a conformational antigen"

CDS

1..>2058
/note="unnamed protein product"
/codon_start=1
/transl_table=11
/protein_id="CAD38232.1"
/db_xref="GI:21714048"
/db_xref="RENTREMBL:CAD38232"
/translations="MAPITAYAOOTRGILGLILITSLTRDKNOVEGEVOIVSTAQTF
LATCINGVCTVHVGACRTIAEPKGVIOYNTVDQDLVGNWPAQSGSLPCTCGS
SDLYLVTRHADVIPIRRGDSRGLSPREISYLNKSGGGLPCPAGHVGIVFRAVC
TRGAKAVDFIPVENLETTMRSPVFTDINSPPVPPQSFQVAHLHPTGSGSKTKVPA
YAAQGYKVLNLSVAATLFGAYMSKAHGINENRTGRTVITITGSPITYSTYKFLA
DGGSGGAYDIIICDECHSDATSLIGITVLDQETAGARLVLAATATPPGVTVP
PNIIEVALSTGTEIPFYKAIPLKVIKGRHLFCHSKKCDLAAKLVALGINAVAY
YRGDLVSVIPPIGDVVVATDALMTGVTGDFDSVIDCNTCTVTQVDPGLDPTFTETI
TLPODAVSRTOGRGTRGKGLYRFVARGERSGMDSSVLCQDAGCAYELVTPA
ETTVRLAYNTPGLPCQDHLFEWEGVTGLTHIDAHFLSQTKQSGENPLVAYQ
TVCARAQAPPSDQMKCLIRKLPILHGTPLLYRLGAVONEITLTHPVTKYIMTCM
SADLEVVSTWLVVGGVLAALAYCLSTGCVIIVGRVLSGRPAIIPDREVLYRFEDE
MEEC"

ORIGIN

Query Match 2.7%; Score 56; DB 6; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 347
Db 292 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 347

RESULT 41

LOCUS 2064 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 69 from patent US 5585258.
ACCESSION I32187
VERSION I32187.1 GI:1822978

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2064)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.

TITLE Hepatitis C virus protease
JOURNAL Patent: US 5585258-A 69 17-DEC-1996;

FEATURES

1..2064
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.7%; Score 56; DB 6; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 347
Db 541 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 596

RESULT 42

LOCUS 2064 bp DNA linear PAT 06-FEB-1997
DEFINITION Sequence 69 from patent US 5585258.
ACCESSION I34278
VERSION I34278.1 GI:1825069

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 2064)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.

TITLE Hepatitis C virus protease
JOURNAL Patent: US 5585258-A 69 17-DEC-1996;

FEATURES

1..2064
Location/Qualifiers
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 2.7%; Score 56; DB 6; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 347
Db 541 TGCACTTGGCGCTCTCGGACCTTTACCTGTCACGAGGACGCCGATGTCATTCC 596

RESULT 43

LOCUS 2064 bp DNA linear PAT 10-JUN-1998
DEFINITION Sequence 69 from patent US 5712145.
ACCESSION I82483
VERSION I82483.1 GI:3210780

KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

Query Match 2.7%; Score 56; DB 6; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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REFERENCE 1 (bases 1 to 2064)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5712145-A 69 27-JAN-1998;
FEATURES Location/Qualifiers
source 1..2064
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 347
Db 541 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 596

RESULT 44
BD140408 2064 bp DNA linear PAT 18-SEP-2002
LOCUS Hepatitis C virus protease.
DEFINITION BD140408
ACCESSION BD140408
VERSION JP 2002051791-A/26.
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

REFERENCE 1 (bases 1 to 2064)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: JP 2002051791-A 26 19-FEB-2002;
COMMENT CHIRON CORP
OS HCV
PN JP 2002051791-A/26
PD 19-FEB-2002
PF 11-JUN-2001 JP 2001176369
PR 04-APR-1990 US 505433
PI MICHAEL HOUGHTON,QUI LIM CHOO,GEORGE KUO
PC C12N15/09,C12N15/09,C12N9/50,C12R1:93),(C12N15/09,
PC C12R1:93),
PC C12N15/00,C12N15/00,(C12N15/00,C12R1:93)
CC Hepatitis C virus protease
FH Key Location/Qualifiers
FT CDS (7)..(2064).

FEATURES
source 1..2064
/organism="Hepatitis C virus"
/mol_type="genomic DNA"
/db_xref="taxon:11103"

ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 347
Db 541 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 596

RESULT 45
BD140416 2283 bp DNA linear PAT 18-SEP-2002
LOCUS Hepatitis C virus protease.
DEFINITION BD140416
ACCESSION BD140416
VERSION JP 2002051791-A/34..
KEYWORDS Hepatitis C virus
SOURCE Hepatitis C virus
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Hepacivirus.

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Hepacivirus.
REFERENCE 1 (bases 1 to 2283)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: JP 2002051791-A 34 19-FEB-2002;
COMMENT CHIRON CORP
OS HCV
PN JP 2002051791-A/34
PD 19-FEB-2002
PF 11-JUN-2001 JP 2001176369
PR 04-APR-1990 US 505433
PI MICHAEL HOUGHTON,QUI LIM CHOO,GEORGE KUO
PC C12N15/09,C12N15/09,C12N9/50,C12R1:93),(C12N15/09,
PC C12R1:93),
PC C12N15/00,C12N15/00,(C12N15/00,C12R1:93)
CC Hepatitis C virus protease
FH Key Location/Qualifiers
FT CDS (1)..(2283)
FT mat_peptide (466)..

FEATURES
source 1..2283
Location/Qualifiers
/organism="Hepatitis C virus"
/mol_type="genomic DNA"
/db_xref="taxon:11103"

ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 2283;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 347
Db 1000 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 1055

RESULT 46
I32195 2523 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 85 from patent US 5585259.
DEFINITION I32195
ACCESSION I32195
VERSION I32195.1 GI:1822986
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2523)
AUTHORS Houghton,M., Choo,Q.-L. and Kuo,G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5585259-A 85 17-DEC-1996;
FEATURES Location/Qualifiers
source 1..2523
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 2.7%; Score 56; DB 6; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 347
Db 1000 TGCACCTTCGGCTCCTCGGACCTTACCTGTGTACAGGACGCGCGATGTCATTC 1055

RESULT 47
I34286 2523 bp DNA linear PAT 06-FEB-1997
LOCUS Sequence 85 from patent US 5597691.
DEFINITION I34286
ACCESSION I34286
VERSION I34286.1 GI:1825077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

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Unclassified.
1 (bases 1 to 2523)
Houghton, M., Choo, Q.-L. and Kuo, G.
TITLE Hepatitis C virus protease
JOURNAL Patent: US 5597691-A 85 28-JAN-1997;
FEATURES
    source
    1..2523
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN
Query Match      2.7%; Score 56; DB 6; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347
Db      1000 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 1055

RESULT 48
I82491
LOCUS      I82491      2523 bp      DNA      linear      PAT 10-JUN-1998
DEFINITION Sequence 85 from patent US 5712145.
ACCESSION I82491
VERSION   I82491.1 GI:3210788
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 2523)
AUTHORS  Houghton, M., Choo, Q.-L. and Kuo, G.
TITLE    Hepatitis C virus protease
JOURNAL  Patent: US 5712145-A 85 27-JAN-1998;
FEATURES  Location/Qualifiers
    source
    1..2523
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN

Query Match      2.7%; Score 56; DB 6; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347
Db      1000 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 1055

RESULT 49
AR118686
LOCUS      AR118686      5360 bp      DNA      linear      PAT 16-MAY-2001
DEFINITION Sequence 53 from patent US 6150087.
ACCESSION AR118686
VERSION   AR118686.1 GI:14100596
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 5360)
AUTHORS  Chien, D.Y.
TITLE    NANBV diagnostics and vaccines
JOURNAL  Patent: US 6150087-A 53 21-NOV-2000;
FEATURES  Location/Qualifiers
    source
    1..5360
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN

Query Match      2.7%; Score 56; DB 6; Length 5360;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      292 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347
Db      1221 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 1276

RESULT 50
I06434
LOCUS      I06434      5360 bp      DNA      linear      PAT 02-DEC-1994
DEFINITION Sequence 48 from Patent EP 0318216.
ACCESSION I06434
VERSION   I06434.1 GI:590311
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 5360)
AUTHORS  Houghton, M., Choo, Q.-L. and Kuo, G.
TITLE    Nanbv diagnostics and vaccines
JOURNAL  Patent: EP 0318216-A1 48 31-MAY-1989;
FEATURES  Location/Qualifiers
    source
    1..5360
    /organism="unknown"
    /mol_type="unassigned DNA"
ORIGIN

Query Match      2.7%; Score 56; DB 6; Length 5360;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347
Db      1221 TGCACITTCGGCTCCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 1276

Search completed: August 19, 2004, 08:53:50
Job time : 7832 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2004, 03:08:25 ; Search time 782 Seconds
(without alignments)

11196.338 Million cell updates/sec

Title: US-09-930-591-1

Perfect score: 2061

Sequence: 1 atggcgctatcagggccta.....atgaaatggaagagtgtcta 2061

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 3373863 seqs, 2124099041 residues

Word size : 35

Total number of hits satisfying chosen parameters: 209

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- N_Geneseq_29Jan04:*
- 1: Geneseq1980s:*
 - 2: Geneseq1990s:*
 - 3: Geneseq2000s:*
 - 4: Geneseq2001as:*
 - 5: Geneseq2001bs:*
 - 6: Geneseq2002s:*
 - 7: Geneseq2003as:*
 - 8: Geneseq2003bs:*
 - 9: Geneseq2003cs:*
 - 10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061	100.0	2061	6	Aad34500 Hepatitis
2	2061	100.0	2061	6	Aad31767 Hepatitis
3	2061	100.0	2061	9	Aad60868 Hepatitis
4	62	3.0	943	2	Aaq32984 HCV NS3/N
5	62	3.0	943	2	Aax84003 HCV E1
6	62	3.0	943	2	Aax16760 Hepatitis
7	62	3.0	7983	9	Aad93727 Hepatitis
8	62	3.0	9365	6	Aad25518 Hepatitis
9	61	3.0	957	3	Aaz36164 Nucleotid
10	58	2.8	382	2	Aaq38233 HCV-108
11	58	2.8	382	5	Aaf32234 HCV recom
12	58	2.8	1414	2	Aaq38232
13	58	2.8	1414	5	Aaf32233 HCV recom
14	58	2.8	1420	5	Aaq38234 Clone pHc
15	58	2.8	1420	5	Aaf32235 HCV recom
16	56	2.7	281	2	Aaq14299 Hepatitis
17	56	2.7	281	2	Aaq14361
18	56	2.7	281	2	Aaf59255
19	56	2.7	281	2	Aav04988
20	56	2.7	281	2	Aax26393
21	56	2.7	281	8	Acda4791 Hepatitis
22	56	2.7	281	8	Ada07864 Hepatitis
23	56	2.7	282	1	Aan90317 Hepatitis

24	56	2.7	282	2	AAQ80170	Hepatitis
25	56	2.7	283	1	AAQ92087	Sequence
26	56	2.7	368	2	AAQ14297	Hepatitis
27	56	2.7	368	2	AAQ14359	Clone C20
28	56	2.7	368	2	AAQ80168	Hepatitis
29	56	2.7	368	2	AAQ59254	Hepatitis
30	56	2.7	368	2	AAV04986	Nucleotid
31	56	2.7	368	2	AAQ26391	Nucleotid
32	56	2.7	368	8	ACD44789	Hepatitis
33	56	2.7	368	8	ADA07860	Hepatitis
34	56	2.7	612	8	ABX15706	Anti-vira
35	56	2.7	1947	2	AAQ14304	Vector cf
36	56	2.7	2058	6	ABK15344	Hepatitis
37	56	2.7	2058	6	AAQ29795	HCV-1 NS3
38	56	2.7	2058	7	ABX14410	DNA encod
39	56	2.7	2058	9	ADCG6768	HCV mutan
40	56	2.7	2064	2	AAQ14296	Hepatitis
41	56	2.7	2064	2	AAQ80167	Hepatitis
42	56	2.7	2064	2	AAQ59260	DNA encod
43	56	2.7	2064	2	AAV04985	Nucleotid
44	56	2.7	2064	2	AAQ26390	DNA encod
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48	56	2.7	2523	2	AAQ14358	Sequence
49	56	2.7	2523	2	AAQ80175	Hepatitis
50	56	2.7	2523	2	AAQ59261	HCV prote
51	56	2.7	2523	2	AAV04993	cf1SODp60
52	56	2.7	2523	2	AAQ26398	Nucleotid
53	56	2.7	2523	8	ACD44796	Hepatitis
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56	56	2.7	5360	1	AAQ90327	Hepatitis
57	56	2.7	6299	4	AAF83669	HCV NS3/4A
58	56	2.7	6905	1	AAQ92103	Combined
59	56	2.7	7310	1	AAQ92106	Combined
60	56	2.7	7310	1	AAQ90336	Composite
61	56	2.7	7310	2	AAQ98221	Hepatitis
62	56	2.7	8316	2	AAQ05955	Hepatitis
63	56	2.7	8316	3	AAQ75296	CDNA sequ
64	56	2.7	9133	2	AAQ207656	Nucleotid
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66	56	2.7	9185	2	AAQ10566	Hepatitis
67	56	2.7	9185	2	AAQ00459	Hepatitis
68	56	2.7	9185	2	AAQ26737	Nucleotid
69	56	2.7	9185	3	AAQ75297	Sense str
70	56	2.7	9400	2	AAQ21744	Compiled
71	56	2.7	9401	2	AAQ12710	Hepatitis
72	56	2.7	9401	2	AAQ99981	HCV polyyp
73	56	2.7	9401	6	AAQ35043	Hepatitis
74	56	2.7	9401	6	ABL55592	HCV bait
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76	53	2.6	583	6	ABL55593	HCV bait
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79	53	2.6	7989	9	ADD93722	Hepatitis
80	53	2.6	7992	9	ADD93723	Hepatitis
81	53	2.6	9416	2	AAQ22871	NANRV Rut
82	53	2.6	9416	6	AAQ31764	Hepatitis
83	53	2.6	9416	9	AAQ60865	Hepatitis
84	53	2.6	9518	5	AAQ03778	Hepatitis
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86	53	2.6	9518	5	AAQ03808	Hepatitis
87	53	2.6	9518	5	AAQ24833	Infectiou
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98	53	2.6	10803	7	ABX10617	171	41	2.0	308	8	ACD44793	Hepatit
99	53	2.6	10803	9	ADD67945	172	41	2.0	308	8	ADA07868	Hepatit
100	53	2.6	12980	2	AAV59364	173	41	2.0	477	2	AAQ14277	HCV Clon
101	53	2.6	12980	6	ABX87286	174	41	2.0	477	2	AAQ98205	Hepatit
102	53	2.6	12980	6	ABX87286	175	41	2.0	477	2	AAQ98205	Hepatit
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104	52	2.5	885	2	AAQ12543	177	41	2.0	480	1	AAV70548	Insert of
105	52	2.5	885	8	ACC85400	178	41	2.0	480	1	AAV70548	Insert of
106	50	2.4	337	6	ABL55575	179	41	2.0	480	1	AAV70548	Insert of
107	50	2.4	337	3	AAV55443	180	41	2.0	480	1	AAV70548	Insert of
108	50	2.4	442	6	ABL55563	181	41	2.0	495	2	AAQ14302	Hepatit
109	50	2.4	559	6	ABL55596	182	41	2.0	495	2	AAQ14364	Hepatit
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115	50	2.4	1251	5	AAQ38227	188	41	2.0	495	2	AAQ14364	Hepatit
116	48	2.3	5211	4	AAQ21686	189	41	2.0	558	2	AAQ14364	Hepatit
117	48	2.3	9436	2	AAQ63408	190	41	2.0	558	2	AAQ14364	Hepatit
118	47	2.3	9436	2	AAQ63459	191	41	2.0	558	2	AAQ14364	Hepatit
119	44	2.1	492	1	AAQ74770	192	41	2.0	558	2	AAQ14364	Hepatit
120	44	2.1	492	1	AAQ74770	193	41	2.0	558	2	AAQ14364	Hepatit
121	44	2.1	669	6	AAQ92083	194	41	2.0	558	2	AAQ14364	Hepatit
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130	44	2.1	816	2	AAQ14365	203	36	1.7	85	6	ABL55559	Selected
131	44	2.1	816	8	ACD44795	204	35	1.7	267	2	AAQ58473	HCV pepti
132	44	2.1	816	8	ADA07872	205	35	1.7	390	6	ABL55559	HCV bait
133	44	2.1	2055	2	AAV54955	206	35	1.7	453	6	ABL55559	Selected
134	44	2.1	2499	6	AAQ29796	207	35	1.7	475	6	ABL55559	HCV bait
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139	44	2.1	3075	2	AAQ99982							
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141	44	2.1	3297	6	ABX15345							
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144	44	2.1	8451	7	AAQ14423							
145	44	2.1	9379	2	AAQ14423							
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149	44	2.1	9416	7	ACA62483							
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153	44	2.1	9622	7	AAQ33282							
154	44	2.1	19798	4	AAQ33282							
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157	44	2.1	20217	4	AAQ33282							
158	44	2.1	20247	4	AAQ33282							
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160	43	2.1	347	1	AAQ90318							
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164	41	2.0	268	1	AAQ90311							
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166	41	2.0	308	2	AAQ14301							
167	41	2.0	308	2	AAQ14363							
168	41	2.0	308	2	AAQ80172							
169	41	2.0	308	2	AAQ59252							
					AAV04990							

ALIGNMENTS

RESULT 1
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 ID AAD34500 standard; DNA; 2061 BP.
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 AC AAD34500;
 DT 16-JUL-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/4A protein encoding DNA.
 KW Hepatitis C virus; HCV; NS3/4A protein; therapy; HCV infection; vaccine;
 KW virucide; gene; ds.
 OS Hepatitis C virus.
 XX
 FT Key Location/Qualifiers
 CDS 1..2061
 /tag= a
 /product= "HCV NS3/4A protein"
 XX WO200214362-A2.
 PN 21-FEB-2002.
 PD 15-AUG-2001; 2001WO-IB001774.
 XX 17-AUG-2000; 2000US-0225767P.
 PR 29-AUG-2000; 2000US-0229175P.

1741 CAGATGTGGAAGTGTGATCGCTCTCAAGCCCAACCCCTCCATGGGGCAACACCTCTGTCTA 1800
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 1921 GTTCTGGCTCTTTGGCGCGGTATTCCTATCCAGAGTACCTGGGTGCTGCTGCTGCTGCTG 1980
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 1981 ATTGCTGTGCGGAAGCGGCAATCATACCCGACAGGAGTCTCTACCGGAGTTC 2040
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 2041 GATGAATGGAAGTGTCTGA 2061
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 ID AAD31767 standard; DNA; 2061 BP.
 AC AAD31767;
 XX
 XX 18-JUN-2002 (first entry)
 DE Hepatitis C virus (HCV) NS3/4A DNA coding region.
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 XX Hepatitis C virus; HCV infection; virucide; fungicide; antibacterial;
 KW cyrostatic; immunostimulant; vaccine; ribavirin; immune response; cancer;
 KW ds.
 XX
 XX Hepatitis C virus.
 OS
 XX
 XX Key Location/Qualifiers
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 XX
 XX WO200213855-A2.
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 XX 21-FEB-2002.
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 XX 15-AUG-2001; 2001WO-IB001808.
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 XX 17-AUG-2000; 2000US-0225767P.
 XX 29-AUG-2000; 2000US-0229175P.
 XX 03-NOV-2000; 2000US-00705547.
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 XX (TRIP-) TRIPPE AB.
 XX
 XX Sallberg M, Hultgren C;
 FI WPI; 2002-241837/29.
 XX
 XX P-PSDB; AAE19900.
 XX
 XX Vaccine compositions for treating and preventing disease, preferably
 PT hepatitis C virus infection, comprises ribavirin and antigen that has
 FT epitope present in hepatitis C virus.
 XX
 XX Claim 1; Page 94-95; 120pp; English.
 XX
 XX The invention relates to a composition comprising ribavirin and an
 CC antigen preferably non structural 3 protein (NS3)/4A fragment of
 CC hepatitis C virus (HCV) genome or a peptide or nucleic acid of HCV
 CC sequence. The composition is useful for enhancing an immune response to a
 CC hepatitis C antigen in humans, domestic, sport or pet species and as
 CC vaccines for treating and preventing HCV infections. The composition is

CC also useful for treating viral, bacterial, fungal diseases and cancer.
 CC The present sequence is HCV NS3/4A DNA coding region
 XX
 SQ Sequence 2061 BP; 427 A; 616 C; 571 G; 447 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2061; DB 6; Length 2061;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 1981 ATTGTCTTGTCCGAAAGCGGCAATCATACCGCAAGGGAAGTCTCTTACCGGAGTTC 2040
 Db 1981 ATTGTCTTGTCCGAAAGCGGCAATCATACCGCAAGGGAAGTCTCTTACCGGAGTTC 2040
 QY 2041 GATGAATGGAAGAGTCTCTGA 2061

Db 2041 GATGAATGGAAGAGTCTCTGA 2061
 RESULT 3
 AAD60868
 ID AAD60868 standard; DNA; 2061 BP.
 AC AAD60868;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Hepatitis C virus NS3/4A DNA.
 XX
 KW Ribavirin; vaccine; immune response; infection; therapy; immunostimulant;
 KW virucide; ds.
 XX
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..2061
 FT /*tag= a
 FT /product= "Hepatitis C virus protein"
 XX
 US2002136740-A1.
 PN 26-SEP-2002.
 XX
 PD 26-SEP-2002.
 XX
 PF 15-AUG-2001; 2001US-00929955.
 XX
 PR 17-AUG-2000; 2000US-0225767P.
 PR 29-AUG-2000; 2000US-0229175P.
 XX
 PA (SALL/) SALLBERG M.
 PA (HULT/) HULTGREN C.
 XX
 PI Sallberg M, Hultgren C;
 DR WPI: 2003-764978/72.
 DR P-PSDB; ABW00351.
 XX
 PT Vaccine compositions for treating and preventing disease, preferably
 PT hepatitis C virus infection, comprises ribavirin and antigen that has
 PT epitope present in hepatitis C virus.
 PS Claim 1: Page 60-61; Opp; English.
 CC The invention relates to a composition comprising ribavirin and an
 CC antigen, where the antigen is derived from a hepatitis virus. The vaccine
 CC is useful in enhancing the immune response to a hepatitis C antigen where
 CC the composition is delivered to an animal identified as requiring an
 CC enhanced immune response. The vaccine is useful in the treatment and
 CC prevention of hepatitis C infection. The present sequence is Hepatitis C
 CC virus NS3/4A DNA
 SQ Sequence 2061 BP; 427 A; 616 C; 571 G; 447 T; 0 U; 0 Other;
 Query Match 100.0%; Score 2061; DB 9; Length 2061;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2061; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATGGCGCTTATCAGCGCTATGCCAGCAGACAGAGGCGCTTTGGGATGCATATCACC 60
 Db 1 ATGGCGCTTATCAGCGCTATGCCAGCAGACAGAGGCGCTTTGGGATGCATATCACC 60
 QY 61 ACCTTGACCGCGCGGACAAACACAGGTGAGGTTCAGATCGTGTCAACTGCT 120
 Db 61 ACCTTGACCGCGCGGACAAACACAGGTGAGGTTCAGATCGTGTCAACTGCT 120
 QY 121 GCCCAGACTTTCTTGGCAACCTGCAATTAACGGGGTGTGTGGACTGTCTACCATGAGCC 180
 Db 121 GCCCAGACTTTCTTGGCAACCTGCAATTAACGGGGTGTGTGGACTGTCTACCATGAGCC 180

QY	181	GGAAACAGGACCAATTGGCTCACTTAAGGTCCTGTTATCCAGATGTACCAATGTGGAC	240
Db	181	GGAAACAGGACCAATTGGCTCACTTAAGGTCCTGTTATCCAGATGTACCAATGTGGAC	240
QY	241	CAAGACCTCGTAGGCTGGCGGCTCCCAAGGTGCGGCTCATTAACACCATGCATTTGC	300
Db	241	CAAGACCTCGTAGGCTGGCGGCTCCCAAGGTGCGGCTCATTAACACCATGCATTTGC	300
QY	301	GGCTTCCTCGAACCTTTACCTGGTCACGAGGACGCGCATCTCATCTGTCGCCGACGG	360
Db	301	GGCTTCCTCGAACCTTTACCTGGTCACGAGGACGCGCATCTCATCTGTCGCCGACGG	360
QY	361	GGTGATGGCAGGGCAGCTGCTTTCCCGCGGCTATCTCTTACTTGAAGGCTCTCTCG	420
Db	361	GGTGATGGCAGGGCAGCTGCTTTCCCGCGGCTATCTCTTACTTGAAGGCTCTCTCG	420
QY	421	GGAGGCCCTCTGCTGTGCCCCGAGGACATGCCGTAGGCATATTCAGAGCGCGGTATGC	480
Db	421	GGAGGCCCTCTGCTGTGCCCCGAGGACATGCCGTAGGCATATTCAGAGCGCGGTATGC	480
QY	481	ACCCGTGGAGTGGCTAAGCGGTGGACTTCATCCCGTAGAGAGCTTAGAGACAACCATG	540
Db	481	ACCCGTGGAGTGGCTAAGCGGTGGACTTCATCCCGTAGAGAGCTTAGAGACAACCATG	540
QY	541	AGGTCCCGGTGTTCTCAGACAACCTCTCCCAAGGCTGCCCCAGAGCTTACCAAGTG	600
Db	541	AGGTCCCGGTGTTCTCAGACAACCTCTCCCAAGGCTGCCCCAGAGCTTACCAAGTG	600
QY	601	GCCCACTGTCATGCTCCCAAGGCTGAGGCTAAGAGCAACCAAGTCCCGCGCATACGCA	660
Db	601	GCCCACTGTCATGCTCCCAAGGCTGAGGCTAAGAGCAACCAAGTCCCGCGCATACGCA	660
QY	661	GCTCAGGGCTACAGGTGCTGGTCTCAACCCCTCGTCTGCTGCAACATGGGCTTTGGT	720
Db	661	GCTCAGGGCTACAGGTGCTGGTCTCAACCCCTCGTCTGCTGCAACATGGGCTTTGGT	720
QY	721	GCTTACATGTCACAGGCTGAGTGTATCCAAATCAGAGCTGGGGTGAGGACAAT	780
Db	721	GCTTACATGTCACAGGCTGAGTGTATCCAAATCAGAGCTGGGGTGAGGACAAT	780
QY	781	ACTACTGGCAGCCGATCAGCTATTCACCTACGGGAAAGTTCCTGCGCAGCGGGTGT	840
Db	781	ACTACTGGCAGCCGATCAGCTATTCACCTACGGGAAAGTTCCTGCGCAGCGGGTGT	840
QY	841	TCAGGGGTGCTTATGACATAAATTTGTGACAGTGCCACTCCACGGATGCAACATCC	900
Db	841	TCAGGGGTGCTTATGACATAAATTTGTGACAGTGCCACTCCACGGATGCAACATCC	900
QY	901	ATCTTGGGCATTTGGCACTGTCTTGACCAAGCAGAGACCGCGGGGCGAGACTGTGTG	960
Db	901	ATCTTGGGCATTTGGCACTGTCTTGACCAAGCAGAGACCGCGGGGCGAGACTGTGTG	960
QY	961	CTCGCCACCGCTACCCCTCGGGCTCGTCACTGTGCCCATCTTAACATCGAGGAGTT	1020
Db	961	CTCGCCACCGCTACCCCTCGGGCTCGTCACTGTGCCCATCTTAACATCGAGGAGTT	1020
QY	1021	GCTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGCTATTCCTTTGAAGCAAT	1080
Db	1021	GCTCTGTCCACTACCGGAGAGATCCCTTTTATGGCAAGCTATTCCTTTGAAGCAAT	1080
QY	1081	AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAGAGTGGCAGGCTCGCGCA	1140
Db	1081	AAGGGGGGAGACATCTCATCTTCTGCACTCAAGAGAGTGGCAGGCTCGCGCA	1140
QY	1141	AAACTGTGCGGTGGGGCTCAATCCGCTGCTTACTACCGCGGCTTGATGTGCGTC	1200
Db	1141	AAACTGTGCGGTGGGGCTCAATCCGCTGCTTACTACCGCGGCTTGATGTGCGTC	1200
QY	1201	ATCCCGACCAAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTACC	1260
Db	1201	ATCCCGACCAAGTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTTACC	1260
QY	1261	GGCGACTTCGATTCGGTGTAGAGCTGCAACACGCTGTGTACCCAGACAGTCGACTTCAGC	1320

Db	1261	GGCGACTTCGATTCGGTGTAGAGCTGCAACACGCTGTGTACCCAGACAGTCGACTTCAGC	1320
QY	1321	CTTGACCTCTACCTTCAACCATTTAGACATACAGCTTCCCAAGGATGCTGTCTCCGTA	1380
Db	1321	CTTGACCTCTACCTTCAACCATTTAGACATACAGCTTCCCAAGGATGCTGTCTCCGTA	1380
QY	1381	CAACGTCGGGTAGGACTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1440
Db	1381	CAACGTCGGGTAGGACTGGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1440
QY	1441	GAGCGCTCTTCTGGCATTTTGTGCTGCTCTCTGCGAGTGTATGACGCGGGTGT	1500
Db	1441	GAGCGCTCTTCTGGCATTTTGTGCTGCTCTCTGCGAGTGTATGACGCGGGTGT	1500
QY	1501	GCTTGGTATGAGCTTACGCGCGGAGACACAGCTTAGGCTACGAGCATACATGAACACC	1560
Db	1501	GCTTGGTATGAGCTTACGCGCGGAGACACAGCTTAGGCTACGAGCATACATGAACACC	1560
QY	1561	CGGGACTTCCCGTGTGCCAAGACCACTTCTTGAATTTGGAGGGGCTTTTACGGGTCTC	1620
Db	1561	CGGGACTTCCCGTGTGCCAAGACCACTTCTTGAATTTGGAGGGGCTTTTACGGGTCTC	1620
QY	1621	ACCCACATAGACGCGCCACTTCTTATCCAGACAAAGCAGAGTGGGGAACCTTCCCTAT	1680
Db	1621	ACCCACATAGACGCGCCACTTCTTATCCAGACAAAGCAGAGTGGGGAACCTTCCCTAT	1680
QY	1681	CTGTAGGCTTACCAAGCACCCTGTGCGCTAGAGCTCAAGCCCTCCCGCTGCTGGGAC	1740
Db	1681	CTGTAGGCTTACCAAGCACCCTGTGCGCTAGAGCTCAAGCCCTCCCGCTGCTGGGAC	1740
QY	1741	CAGATGTGGAAGTGTGATCCGCTCTCAAGCCCACTTCCATGGGCGCAACACCTTCTGTA	1800
Db	1741	CAGATGTGGAAGTGTGATCCGCTCTCAAGCCCACTTCCATGGGCGCAACACCTTCTGTA	1800
QY	1801	TATAGCTGGGCGGTGTCAGAGTGAAGTCACTGACGCAACCCAGTCAACCAAGTATATC	1860
Db	1801	TATAGCTGGGCGGTGTCAGAGTGAAGTCACTGACGCAACCCAGTCAACCAAGTATATC	1860
QY	1861	ATGACATGATGTGGGTGACCTGAGGTGCTGACGAGTACCTGGGTCTGTTGGCGGC	1920
Db	1861	ATGACATGATGTGGGTGACCTGAGGTGCTGACGAGTACCTGGGTCTGTTGGCGGC	1920
QY	1921	GTTCTGGCTGTTGGCGCGTATTTGCTATCCACAGGCTCGGTGCTAGTAGTAGG	1980
Db	1921	GTTCTGGCTGTTGGCGCGTATTTGCTATCCACAGGCTCGGTGCTAGTAGTAGG	1980
QY	1981	ATTGCTTGTCCGGAAGCGGCAATCATCCGACAGGGAAGTCTCTACCGGGAGTTC	2040
Db	1981	ATTGCTTGTCCGGAAGCGGCAATCATCCGACAGGGAAGTCTCTACCGGGAGTTC	2040
QY	2041	GATGAATGGAAGAGTGTCTGA 2061	
Db	2041	GATGAATGGAAGAGTGTCTGA 2061	

RESULT 4
AAQ32984
ID AAQ32984 standard; DNA; 943 BP.
XX
AC AAQ32984;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 14-MAY-1993 (first entry)
XX
DE HCV NS3/NS4 non-structural region.
XX
XX PCR; amplification; prototype; HCV pr; ss.
XX Hepatitis C virus; HCVel.
XX
FH Key Location/Qualifiers

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FT CDS      2..1210
PT          /*tag= a
XX          /label= NS3/NS4
XX
XX WO9221759-A1.
XX 10-DEC-1992.
XX
XX 04-JUN-1992; 92WO-FR000501.
XX
XX 06-JUN-1991; 91FR-00006882.
XX
XX (INSP ) INST PASTEUR.
XX
XX Brechot C, Kreamsdorf D, Porchon C;
XX WPI; 1992-433657/52.
XX
XX New nucleotide and peptide sequences - specific for French isolate of
PT hepatitis C virus and useful in diagnosing and treating related
PT infections.
XX
XX Disclosure; Fig 8; 50pp; French.
XX
XX RNA was extracted from the serum of an HCV-positive blood donor, subjected
XX to reverse transcription and the cDNA formed amplified by PCR.
XX Amplification prods. were cloned, screened with a probe derived from the
XX HCV prototype and inserts sequenced. The results showed marked
XX conservation in the non-coding region, significant variability in the
XX structural region (encoding envelope proteins) and reduced variability in
XX the non-structural region. The NS3/NS4 coding region corresponds to
XX positions 4361-5303 of HCV prototype (HCV pt) (WO-A-90/14436). (Updated
XX on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to
XX standardise OS field)
XX
XX Sequence 943 BP; 204 A; 292 C; 256 G; 191 T; 0 U; 0 Other;
XX
XX Query Match      3.0%; Score 62; DB 2; Length 943;
XX Best Local Similarity 100.0%; Pred. No. 8.5e-21;
XX Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1915 GCGCGCTTCTGGCTTTGGCGCGTATTGCTATCCACAGCTGCGTGCATAGTA 1974
XX      |||||
XX Db 630 GCGCGCTTCTGGCTTTGGCGCGTATTGCTATCCACAGCTGCGTGCATAGTA 689
XX
XX QY 1975 GG 1976
XX      ||
XX Db 690 GG 691
XX
XX RESULT 5
XX AAX84003
XX ID AAX84003 standard; cDNA; 943 BP.
XX
XX AC AAX84003;
XX
XX DT 27-AUG-2003 (revised)
XX DT 26-AUG-1999 (first entry)
XX
XX DE HCV E1 coding sequence.
XX
XX KW HCV E1 region; monoclonal antibody; diagnosis; HCV E1-specific antigen;
XX KW ss.
XX
XX OS Hepatitis C virus.
XX
XX PN US5919454-A.
XX
XX PD 06-JUL-1999.
XX
XX PF 07-JUN-1995; 95US-00487231.
XX
XX PR 18-MAR-1993; 93US-00965285.

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5,879.904

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XX (INSP ) INST PASTEUR.
XX
XX Porchon C, Brechot C, Kreamsdorf D;
XX
XX WPI; 1999-394595/33.
XX P-PSDB; AAY22022.
XX
XX Nucleotides and peptides from hepatitis C virus isolate for detecting E1-
PT specific antigens.
XX
XX Disclosure; Col 15-18; 45pp; English.
XX
XX This sequence encodes a hepatitis c virus (HCV) E1 region protein. The
XX invention relates to human or murine monoclonal antibodies directed
XX against a HCV E1 protein sequence. The monoclonal antibodies and their
XX fragments are useful for the in vitro diagnosis of HCV E1-specific
XX antigens. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX Sequence 943 BP; 204 A; 292 C; 256 G; 191 T; 0 U; 0 Other;
XX
XX Query Match      3.0%; Score 62; DB 2; Length 943;
XX Best Local Similarity 100.0%; Pred. No. 8.5e-21;
XX Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1915 GCGCGCTTCTGGCTTTGGCGCGTATTGCTATCCACAGCTGCGTGCATAGTA 1974
XX      |||||
XX Db 630 GCGCGCTTCTGGCTTTGGCGCGTATTGCTATCCACAGCTGCGTGCATAGTA 689
XX
XX QY 1975 GG 1976
XX      ||
XX Db 690 GG 691
XX
XX RESULT 6
XX AAX16760
XX ID AAX16760 standard; cDNA to mRNA; 943 BP.
XX
XX AC AAX16760;
XX
XX DT 27-APR-1999 (first entry)
XX
XX DE Hepatitis C virus NS3/NS4 region.
XX
XX KW E1 region; French Hepatitis C virus; HCV; immunogen; antibody; detection;
XX KW immunoassay; ss.
XX
XX OS Hepatitis C virus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 3..941
XX FT /*tag= a
XX FT /product= "NS3/NS4 protein"
XX FT /note= "no start or stop codons are given at the 5' or 3'
XX FT ends of the sequence"
XX
XX PN US5866139-A.
XX
XX PD 02-FEB-1999.
XX
XX PF 07-JUN-1995; 95US-00483695.
XX
XX PR 18-MAR-1993; 93US-00965285.
XX
XX (INSP ) INST PASTEUR.
XX
XX Porchon C, Kreamsdorf D, Brechot C;
XX
XX WPI; 1999-141865/12.
XX P-PSDB; AAW75483.
XX
XX New isolated and purified Hepatitis C virus E1 peptides - useful for
PT vaccine production or diagnostic purposes.

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XX Disclosure; Col 15-18; 45pp; English.

XX The sequence represents the NS3/NS4 region from a French Hepatitis C virus (HCV) isolate. The encoded protein or peptides derived from it can be: (i) conjugated to a carrier protein and used as immunogens for eliciting protective antibodies; or (ii) labelled, and used as immunoassay reagents for detecting antibodies specific for HCV E1

XX Sequence 943 BP; 204 A; 292 C; 256 G; 191 T; 0 U; 0 Other;

Query Match 3.0%; Score 62; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 8.5e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1915 GCGCGGTTCTGGTCTTTGCGCGCGTATTGCTATCCACAGCTCGTGGTCAATAGTA 1974
|||
DB 630 GCGCGGTTCTGGTCTTTGCGCGCGTATTGCTATCCACAGCTCGTGGTCAATAGTA 689
|||

QY 1975 GG 1976
||
DB 690 GG 691

RESULT 7
ADD93727
ID ADD93727 standard; DNA; 7983 BP.

XX AC ADD93727;

XX DT 29-JAN-2004 (first entry)

XX DE Hepatitis C virus genotype 1a replicon.

XX KW HCV; vaccine; virucide; ss.

XX OS Hepatitis C virus; genotype 1a.

XX PN WO2003085084-A2.

XX PD 16-OCT-2003.

XX PF 03-APR-2003; 2003WO-US010177.

XX PR 03-APR-2002; 2002US-0369685P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Gates A, Gu B, Sarisky RT;

XX WPI; 2003-804301/75.

XX New hepatitis C virus (HCV) sub-genomic replicon, useful for facilitating screening or testing of anti-HCV drugs, comprises a nucleic acid construct encoding chimeric HCV non-structural proteins, and an NS5B polymerase gene.

XX Claim 16; Page 51-56; 159pp; English.

XX The present sequence comprises a replicating hepatitis C virus (HCV) genotype 1a replicon. The invention provides sub-genomic replicons of HCV comprising a nucleic acid construct encoding chimeric HCV nonstructural protein and an NS5B polymerase gene. A preferred replicon comprises an NS3 nucleotide sequence ADD93721 that encodes the first 75 contiguous N-terminal amino acids of the NS3 of genotype 1b, of a BB7 strain. A chimeric replicon may comprise an NS3 sequence, from any of the 6 major HCV genotypes and subtypes but has its first 225 nucleotides of the coding sequence replaced by the BB7 strain NS3 sequence, especially where the replicon is from HCV genotype 1a (H77 strain) or genotype 1b (J4 strain). Stable cell lines expressing and replicating functional replicons containing sequences from HCV genotype 1a (strain H77) or genotype 1b (strain J4) within the prototype 1b replicon backbone from HCV strain BB7 are provided. These can be used to screen for compounds

CC that modulate viral replication. The sub-genomic HCV replicon systems of the invention may provide the foundation for generating HCV replicons of all 6 major genotypes and subtypes to facilitate screening, testing and evaluating anti-infective agents for HCV disease(s).

XX Sequence 7983 BP; 1630 A; 2385 C; 2235 G; 1733 T; 0 U; 0 Other;

Query Match 3.0%; Score 62; DB 9; Length 7983;
Best Local Similarity 100.0%; Pred. No. 8.1e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 970 GTATCCCTCCGGCTCGTCACTGTGCCCATCTAATCATCGAGGTTGCTCTGTCC 1029
|||
DB 2770 GTATCCCTCCGGCTCGTCACTGTGCCCATCTAATCATCGAGGTTGCTCTGTCC 2829
|||

QY 1030 AC 1031
||
DB 2830 AC 2831

RESULT 8
AAD25518
ID AAD25518 standard; DNA; 9365 BP.

XX AC AAD25518;

XX DT 26-MAR-2002 (first entry)

XX DE Hepatitis C virus isolate colonel complete DNA genome.

XX KW HCV; hepatitis C virus; cytostatic; cancer; immunosuppressive; virucide; antibacterial; fungicide; protozoicide; antirheumatic; antiinflammatory; antiarthritic; rheumatoid arthritis; neuroprotective; multiple sclerosis; immune response; vasotropic; vaccine; gene therapy; autoimmune disease; vasculitis; ds.

XX OS Hepatitis C virus.

XX PN WO200176643-A1.

XX PD 18-OCT-2001.

XX PF 06-APR-2001; 2001WO-US011372.

XX PR 07-APR-2000; 2000US-0195680P.

XX PA (BAYU) BAYLOR COLLEGE MEDICINE.

XX PI Orson FM, Kinsey BM, Bhogal BS;

XX WPI; 2002-066308/09.

XX Composition for oral delivery of vaccines, comprises expression vector containing antigenic genomic sequence, bound to aggregated protein-polycationic polymer conjugate or suspension.

XX Disclosure; Page 87-90; 145pp; English.

XX The invention relates to a composition comprising an expression vector bound to an aggregated protein-polycationic polymer conjugate or suspension. The expression vector contains a promoter polynucleotide sequence operatively linked to a polynucleotide sequence encoding an antigen which is a fragment of a gene or genome associated with an infectious disease, cancer and autoimmune disease such as rheumatoid arthritis, vasculitis, and multiple sclerosis, pathogenic genomes consisting of bacterium, fungus, protozoa and virus such as human immunodeficiency virus (HIV), herpes simplex virus (HSV), hepatitis C virus (HCV), influenza and respiratory syncytial virus (RSV), and optionally comprising a nucleotide sequence encoding a cytokine (or a cytokine expression vector), is useful for inducing an immune response (systemic and/or mucosal) in an organism. The cytokine expression vector contains a sequence for granulocyte macrophage-colony stimulating factor (GM-CSF) or interleukin-12 (IL-12). The polynucleotide sequences encoding

CC the antigen and the cytokine are under transcriptional control of same or
CC different promoter polynucleotide sequences. The expression vector, as a
CC DNA vaccine is useful for treating a condition in an organism. The
CC present sequence is hepatitis C virus isolate colonel complete DNA genome
CC related to the invention

SQ Sequence 9365 BP; 1863 A; 2835 C; 2674 G; 1993 T; 0 U; 0 Other;
Query Match 3.0%; Score 62; DB 6; Length 9365;
Best Local Similarity 100.0%; Pred. No. 8.1e-21;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 970 GCTACCCCTCGGCTCGTCACTGTCCCATCTTAACTCATGAGAGGTTGCTCTGTCC 1029
DB 4374 GCTACCCCTCGGCTCGTCACTGTCCCATCTTAACTCATGAGAGGTTGCTCTGTCC 4433
QY 1030 AC 1031
DB 4434 AC 4435

RESULT 9
AAZ36164
ID AAZ36164 standard; DNA; 957 BP.
AC AAZ36164;
XX 11-FEB-2000 (first entry)
XX Nucleotide sequence of the mtNFH6NS3 clone B9 fusion protein.
XX HCV; NS3 helicase; HCV subtype 1a; HCV subtype 1b; HCV infection;
XX solid phase immunoassay; HCV antigen; NS3 protease; HCV antibody;
XX passive vaccination; ss.
OS Synthetic.
OS Hepatitis C virus.
PH Key Location/Qualifiers
FT CDS 1..957
FT /*tag= a
FT /product= "mtNFH6NS3 clone B9 fusion protein"
FT misc_feature 1..120
FT /*tag= b
FT /note= "these nucleotides encode the non-NS3 sequence,
FT which is the mtNF fusion partner, the hexanistidine tag
FT and part of the multilinker"
PN WO9954735-A1.
XX 28-OCT-1999.
PD 15-APR-1999; 99WO-EF002547.
XX 17-APR-1998; 98EP-00870087.
XX (INNO-) INNOGENETICS NV.
XX Maertens G, Louwagie J, Bosman A, Sablon E, Zrein M;
XX WPI; 2000-013283/01.
XX P-PSDB; AAY43895.
XX New hepatitis C-virus polypeptide used for treating the infection.
XX Claim 22; Fig 3-1; 66pp; English.

CC The present sequence encodes a fusion protein comprising a Hepatitis C
CC virus (HCV) NS3 protein. The NS3 polypeptides are used in a solid phase
CC immunoassay comprising a HCV antigen (preferably a NS3 helicase or NS3
CC protease protein) in the presence of reducing agent on the solid phase.
CC Use of the reducing agent and purification of the antigen using to HCV
CC sulphonation and desulphonation steps increases its reactivity to HCV

CC antibodies and enables an earlier detection of HCV infection. The assay
CC is used for detecting antibodies raised against the HCV antigen. The
CC polypeptides are used for preventing and treating HCV infection. The
CC polypeptides are also used for diagnosing hepatitis infection. The
CC antibodies to these polypeptides are used for providing passive
CC vaccination

SQ Sequence 957 BP; 211 A; 286 C; 259 G; 201 T; 0 U; 0 Other;
Query Match 3.0%; Score 61; DB 3; Length 957;
Best Local Similarity 100.0%; Pred. No. 2.8e-20;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 710 TCGGCTTTGGTCTTACATGTCACAGGCCCATGGGATTCCTAACATCAGGACTGGG 769
DB 344 TCGGCTTTGGTCTTACATGTCACAGGCCCATGGGATTCCTAACATCAGGACTGGG 403
QY 770 T 770
DB 404 T 404

RESULT 10
AAQ38233
ID AAQ38233 standard; DNA; 382 BP.
XX AAQ38233;
AC AAQ38233;
XX 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX PHCV-108 coding for HCV amino acids 1454-1569.
XX Hepatitis C virus; C100 antigen; CKS fusion protein; CMP-XDO synthetase;
XX immunodot assay; Non-A, non-B hepatitis; PCR; polymerase chain reaction;
XX ss.
XX Hepatitis C virus.
XX WO9304087-A1.
XX 04-MAR-1993.
XX 21-AUG-1992; 92WO-US007187.
XX 21-AUG-1991; 91US-00748566.
XX (ABBO) ABBOTT LAB.
XX Desai SM, Casey JM, Rupprecht KR, Devare SG;
XX WPI; 1993-093940/11.
XX Hepatitis C assay using recombinant C-100 region antigens - for detecting
XX antibodies and antigen in body fluids from individuals exposed to
XX hepatitis C virus.
XX Example 11; Page 74; 206pp; English.

CC Plasmid pHCV-68 (see AAQ38232) was used in the construction of pHCV-72
CC (see AAR33569) which expresses the HCV CKS-200 antigen (HCV amino acids
CC 1192-1931) at high levels in E. coli. An NcoI fragment containing the C100
CC coding region was excised from plasmid pHCV-62 (i.e. a clone expressing
CC the HCV CKS-C100 deletion antigen HCV amino acids 1569-1574 and 1598-
CC 1931). This NcoI fragment was inserted into the NcoI site of pHCV-108
CC (i.e. AAQ38233, HCV amino acids 1454-1569) to create pHCV-68. The
CC ClaI/BamHI fragment of pHCV-68 containing the HCV NS3/C100 coding region
CC was excised and inserted into the ClaI/BamHI sites of pHCV-29 (i.e. a
CC clone expressing HCV CKS-33C antigen). (Updated on 25-MAR-2003 to correct
XX PN field.)
XX Sequence 382 BP; 76 A; 113 C; 101 G; 92 T; 0 U; 0 Other;

Query Match 2.8%; Score 58; DB 2; Length 382;
 Best Local Similarity 100.0%; Pred. No. 9.6e-19;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGACAA 1348
 |||||
 DB 33 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGACAA 90
 |||||

RESULT 11
 AAF32233
 ID AAF32234 standard; DNA; 382 BP.
 AC AAF32234;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE HCV recombinant antigen pHCV-108 amino acid sequence SEQ ID NO:56.
 XX
 DE Hepatitis C virus; HCV; antigen; detection; antibody; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US6172189-B1.
 XX
 PD 09-JAN-2001.
 XX
 PF 02-JUN-1997; 97US-00867611.
 XX
 PR 24-AUG-1990; 90US-00572822.
 XX
 PR 07-NOV-1990; 90US-00614069.
 XX
 PR 21-AUG-1991; 91US-00748561.
 XX
 PR 21-AUG-1991; 91US-00748565.
 XX
 PR 21-AUG-1991; 91US-00748566.
 XX
 PR 19-NOV-1992; 92US-00989843.
 XX
 PR 10-JAN-1994; 94US-00179826.
 XX
 PR 01-MAY-1996; 96US-00646757.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Devare SG, Desai SM, Casey JM, Dailey SH, Dawson GJ;
 PI Gutierrez RA, Lesniewski RR, Stewart JL, Rupprecht KR;
 XX
 DR WPI; 2001-122352/13.
 XX
 XX New recombinant antigens representing distinct antigenic regions of
 PT Hepatitis C virus (HCV) genome, useful for detection of antibodies and
 PT antigens in body fluids of individuals exposed to HCV.
 XX
 FS Example 17; Col 203-204; 167pp; English.
 XX
 XX The present invention describes recombinant Hepatitis C virus (HCV)
 CC antigens (I). (I) is useful as a reagent for the detection of antibodies
 CC and antigen in body fluids from individuals exposed to HCV. The HCV assay
 CC uses reliable and efficient reagents and methods to accurately detect the
 CC presence of HCV antibodies in samples obtained from individuals suspected
 CC of having HCV infection. AAF32218 to AAF32235, AAB51371 to AAB51379 and
 CC AAB69001 to AAB69032 represent sequences used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 382 BP; 76 A; 113 C; 101 G; 92 T; 0 U; 0 Other;

Query Match 2.8%; Score 58; DB 5; Length 382;
 Best Local Similarity 100.0%; Pred. No. 9.6e-19;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGACAA 1348
 |||||
 DB 33 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGACAA 90
 |||||

RESULT 12
 AAQ38232

ID AAQ38232 standard; DNA; 1414 BP.
 XX
 AC AAQ38232;
 XX
 DT 25-MAR-2003 (revised)
 DT 01-JUL-1993 (first entry)
 XX
 DE CKS-HCV antigen fusion gene pHCV-68.
 XX
 XX Hepatitis C virus; C100 antigen; CKS fusion protein; CMP-KDO synthetase;
 KW immunodot assay; Non-A, non-B hepatitis; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN WO9304087-A1.
 XX
 PD 04-MAR-1993.
 XX
 XX 21-AUG-1992; 92WO-US007187.
 PF
 XX
 XX 21-AUG-1991; 91US-00748566.
 PR
 XX
 XX (ABBO) ABBOTT LAB.
 XX
 XX Desai SM, Casey JM, Rupprecht KR, Devare SG;
 PI
 XX
 XX WPI; 1993-093940/11.
 DR
 XX
 XX Hepatitis C assay using recombinant C-100 region antigens - for detecting
 PT antibodies and antigen in body fluids from individuals exposed to
 PT hepatitis C virus.
 XX
 XX Example 1; Page 61-62; 206pp; English.
 XX
 XX Plasmid pHCV-68 was used in the construction of pHCV-72 (see AAR33569)
 CC which expresses the HCV CKS-200 antigen (HCV amino acids 1192-1931) at
 CC high levels in E.coli. An NcoI fragment containing the C100 coding region
 CC was excised from plasmid pHCV-62 (i.e. a clone expressing the HCV CKS-
 CC C100 deletion antigen HCV amino acids 1569-1574 and 1598-1931). This NcoI
 CC fragment was inserted into the NcoI site of pHCV-108 (i.e. HCV amino
 CC acids 1454-1569) to create pHCV-68. The ClaI/BamHI fragment of pHCV-68
 CC containing the HCV NS3/C100 coding region was excised and inserted into
 CC the ClaI/BamHI sites of pHCV-29 (i.e. a clone expressing HCV CKS-33C
 CC antigen). (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1414 BP; 244 A; 395 C; 387 G; 388 T; 0 U; 0 Other;

Query Match 2.8%; Score 58; DB 2; Length 1414;
 Best Local Similarity 100.0%; Pred. No. 9.3e-19;
 Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGACAA 1348
 |||||
 DB 22 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTGACCTTACCTTCACCATTTGAGACAA 79
 |||||

RESULT 13
 AAF32233
 ID AAF32233 standard; DNA; 1414 BP.
 XX
 AC AAF32233;
 XX
 DT 17-APR-2001 (first entry)
 XX
 DE HCV recombinant antigen pHCV-68 amino acid sequence SEQ ID NO:51.
 XX
 DE Hepatitis C virus; HCV; antigen; detection; antibody; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US6172189-B1.
 XX
 XX 09-JAN-2001.

XX PF 02-JUN-1997; 97US-00667611.
XX PR 24-AUG-1990; 90US-00572822.
XX PR 07-NOV-1990; 90US-00614069.
XX PR 21-AUG-1991; 91US-00748561.
XX PR 21-AUG-1991; 91US-00748565.
XX PR 21-AUG-1991; 91US-00748566.
XX PR 19-NOV-1992; 92US-00989843.
XX PR 10-JAN-1994; 94US-00179896.
XX PR 01-MAY-1996; 96US-00646757.
XX PA (ABBO) ABBOTT LAB.
XX PI Devare SG, Desai SM, Casey JM, Dailey SH, Dawson GJ;
XX PI Gutierrez RA, Lesniewski RR, Stewart JL, Rupprecht KR;
XX DR WPI; 2001-122352/13.
XX PT New recombinant antigens representing distinct antigenic regions of
XX PT Hepatitis C virus (HCV) genome, useful for detection of antibodies and
XX PT antigens in body fluids of individuals exposed to HCV.
XX PS Example 17; Col 185-188; 167pp; English.
XX CC The present invention describes recombinant Hepatitis C virus (HCV)
XX CC antigens (I). (I) is useful as a reagent for the detection of antibodies
XX CC and antigen in body fluids from individuals exposed to HCV. The HCV assay
XX CC uses reliable and efficient reagents and methods to accurately detect the
XX CC presence of HCV antibodies in samples obtained from individuals suspected
XX CC of having HCV infection. AAF32218 to AAF32235, AAF51371 to AAF51379 and
XX CC AAB69001 to AAB69032 represent sequences used in the exemplification of
XX CC the present invention
XX CC
XX SQ Sequence 1414 BP; 244 A; 395 C; 387 G; 388 T; 0 U; 0 Other;
Query Match 2.8%; Score 58; DB 5; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCTTGACCTTGACCTTACCTTACCATTTGAGACAA 1348
Db 22 ACGTGTGTCACCCAGACAGTCGACTTCAGCTTGACCTTGACCTTACCTTACCATTTGAGACAA 79
RESULT 14
AAQ38234
ID AAQ38234 standard; DNA; 1420 BP.
AC AAQ38234;
XX 25-MAR-2003 (revised)
DT 01-JUL-1993 (first entry)
XX Clone pHCV-69 containing the HCV NS3/C100 coding region.
XX Hepatitis C virus; C100 antigen; CKS fusion protein; CMP-KDO synthetase;
XX immunodot assay; Non-A, non-B hepatitis; PCR; polymerase chain reaction;
XX ss.
XX Hepatitis C virus.
XX OS
XX WO9304087-A1
XX 04-MAR-1993.
XX 21-AUG-1992; 92WO-US007187.
XX 21-AUG-1991; 91US-00748566.
XX (ABBO) ABBOTT LAB.
XX Desai SM, Casey JM, Rupprecht KR, Devare SG;

XX WPI; 1993-093940/11.
XX Hepatitis C assay using recombinant C-100 region antigens - for detecting
XX PT antibodies and antigen in body fluids from individuals exposed to
XX PT hepatitis C virus.
XX PS Example 11; Page 74-75; 206pp; English.
XX CC Plasmid pHCV-69 (i.e. AAQ38234) was used in the construction of pHCV-73
XX CC (see AAR33570) which expresses the HCV CKS-200 antigen (HCV amino acids
XX CC 1192-1599 and 1621-1931) at high levels in E.coli. The C100 coding region
XX CC was excised from plasmid pHCV-63 and inserted into pHCV-108 (i.e.
XX CC AAQ38233, HCV amino acids 1454-1569) to create pHCV-69. The Clai/BamHI
XX CC fragment of pHCV-69 containing the HCV NS3/C100 coding region was excised
XX CC and inserted into the Clai/BamHI sites of pHCV-29 (i.e. a clone
XX CC expressing HCV CKS-33C antigen). (Updated on 25-MAR-2003 to correct PN
XX CC field.)
XX SQ Sequence 1420 BP; 246 A; 396 C; 384 G; 394 T; 0 U; 0 Other;
Query Match 2.8%; Score 58; DB 2; Length 1420;
Best Local Similarity 100.0%; Pred. No. 9.3e-19;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCTTGACCTTGACCTTACCTTACCATTTGAGACAA 1348
Db 22 ACGTGTGTCACCCAGACAGTCGACTTCAGCTTGACCTTGACCTTACCTTACCATTTGAGACAA 79
RESULT 15
AAF32235
ID AAF32235 standard; DNA; 1420 BP.
XX AAF32235;
XX 17-APR-2001 (first entry)
DT
XX HCV recombinant antigen pHCV-59 amino acid sequence SEQ ID NO:57.
DE HCV recombinant antigen pHCV-59 amino acid sequence SEQ ID NO:57.
XX Hepatitis C virus; HCV; antigen; detection; antibody; ss.
OS Hepatitis C virus.
XX US6172189-B1.
XX 09-JAN-2001.
XX 02-JUN-1997; 97US-00867611.
XX 24-AUG-1990; 90US-00572822.
XX 07-NOV-1990; 90US-00614069.
XX 21-AUG-1991; 91US-00748561.
XX 21-AUG-1991; 91US-00748565.
XX 21-AUG-1991; 91US-00748566.
XX 19-NOV-1992; 92US-00989843.
XX 10-JAN-1994; 94US-00179896.
XX 01-MAY-1996; 96US-00646757.
XX (ABBO) ABBOTT LAB.
XX Devare SG, Desai SM, Casey JM, Dailey SH, Dawson GJ;
XX PI Gutierrez RA, Lesniewski RR, Stewart JL, Rupprecht KR;
XX WPI; 2001-122352/13.
XX New recombinant antigens representing distinct antigenic regions of
XX PT Hepatitis C virus (HCV) genome, useful for detection of antibodies and
XX PT antigens in body fluids of individuals exposed to HCV.
XX PS Example 17; Col 203-204; 167pp; English.
XX CC The present invention describes recombinant Hepatitis C virus (HCV)

KW HCV; NS3; non-structural domain 3; protease; polyprotein; inhibitor;
XX screen; processing; infection; treatment; probe; hepatitis C virus; ss.
OS Hepatitis C virus; Virus.
XX
XX U95585258-A.
XX 17-DEC-1996.
XX
XX 06-DEC-1994; 94US-00350884.
XX
XX 04-APR-1990; 90US-00505433.
PR 04-APR-1991; 91US-00680296.
XX
XX (CHIR) CHIRON CORP.
XX
XX Choo Q, Kuo G, Houghton M;
PI WPI; 1997-051175/05.
XX P-PSDB; AAW01691.
XX
XX Compsn. contg. hepatitis C virus NS3 domain protease and related fusion
PT proteins - useful for screening specific inhibitors, potential antiviral
PT agents, prepn. of antibodies and for cleaving specific poly(peptide)s.
XX
XX Example 3; Col 65-68; 68pp; English.
XX
XX Compsn. comprising the hepatitis C virus (HCV) NS3 domain protease or
XX its active truncation analogues are claimed. Also new are fusion proteins
CC comprising the protease (or analogues) and, e.g. human superoxide (SOD)
CC or ubiquitin. The protease is essential for polyprotein processing, and
CC thus infectivity, in HCV. The compsns. are used to screen for specific
CC inhibitors (possibly useful as antiviral agents), to generate specific
CC antibodies and to cleave specific polypeptides. HCV cDNA clones (AAV59250
CC - 56 encoding AAW01686-92 resp.) were isolated from HCV genomic library
CC using probes AAT59244-49. The clones were used in the preparation of full
CC length SOD-protease fusion proteins. (Updated on 25-MAR-2003 to correct
CC PP field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 281 BP; 41 A; 89 C; 92 G; 59 T; 0 U; 0 Other;
Query Match 2.7%; Score 56; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTC 347
DB 4 TGCACCTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTC 59
RESULT 19
AAV04988
ID AAV04988 standard; DNA; 281 BP.
XX
XX AAV04988;
XX
XX 27-AUG-2003 (revised)
DT 07-MAY-1998 (first entry)
XX
XX Nucleotide sequence of the Hepatitis c virus (HCV) clone C8h.
DE
XX
XX Protease; HCV; NS3 domain; human superoxide dismutase; fusion protein;
KW ubiquitin; assay; activity; anti-HCV; ss.
XX
XX Hepatitis C virus.
XX
XX Key Location/Qualifiers
FH 1. .279
FT CDS /*tag= a
FT
XX
XX US5712145-A.
XX 27-JAN-1998.
XX

XX 06-SEP-1996; 96US-00709173.
XX
XX 04-APR-1990; 90US-00505433.
PR 04-APR-1991; 91US-00680296.
XX
XX 06-DEC-1994; 94US-00350884.
PR 12-MAY-1995; 95US-00440548.
XX
XX (CHIR) CHIRON CORP.
XX
XX Choo Q, Kuo G, Houghton M;
PI WPI; 1998-119886/11.
XX P-PSDB; AAW46392.
XX
XX Recombinant hepatitis C virus protease - useful in screening drugs for
PT activity against hepatitis C virus.
XX
XX Disclosure; Fig 4; 68pp; English.
XX
XX The present sequence represents the nucleotide sequence of the Hepatitis
CC C virus (HCV) clone C8h. The clone was isolated using hybridisation probe
CC AAV04975. A cDNA fragment encoding protease was isolated from the clone,
CC and cloned into an expression vector to produce a fusion protein with
CC human superoxide dismutase-protease. The HCV protease is believed to
CC cleave itself from the genomic polyprotein. In the absence of protease
CC activity, the HCV polyprotein should remain in its unprocessed form, and
CC thus render the virus non-infectious. Inhibitors of protease activity
CC should therefore also inhibit viral infectivity. The protease can
CC therefore be used for assaying compounds for activity against HCV.
CC (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 281 BP; 41 A; 89 C; 92 G; 59 T; 0 U; 0 Other;
Query Match 2.7%; Score 56; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTC 347
DB 4 TGCACCTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACGCCGATGTCATTC 59
RESULT 20
AAV26393
ID AAV26393 standard; DNA; 281 BP.
XX
XX AAV26393;
XX
XX 26-MAY-1999 (first entry)
DT
XX
XX Nucleotide sequence of HCV protease clone C8h.
DE
XX
XX HCV NS3 protease; truncation analog; HCV control; protease activity;
KW viral infectivity; inactive non-cleaving protease; ss.
XX
XX Hepatitis C virus.
OS
XX US5885799-A.
XX
XX 23-MAR-1999.
XX
XX 06-SEP-1996; 96US-00709177.
XX
XX 04-APR-1990; 90US-00505433.
PR 04-APR-1991; 91US-00680296.
XX
XX 06-DEC-1994; 94US-00350884.
PR 12-MAY-1995; 95US-00440548.
XX
XX (CHIR) CHIRON CORP.
XX
XX Choo Q, Kuo G, Houghton M;
PI
XX

Same as 9115575A

DR WPI: 1999-228536/19.
 DR P-PSDB; AAW97604.
 XX
 PT Preparation of new Hepatitis C Virus NS3 protease - useful for screening
 PT for compounds which inhibit HCV infectivity.
 XX
 PS Example 3; Fig 4; 71pp; English.
 XX
 CC The specification describes a method for making a purified Hepatitis C
 CC virus (HCV) NS3 protease or active truncation analog. If the HCV protease
 CC N-terminal cleavage signal is excluded (so that self-cleavage is
 CC prevented), the HCV protease remains in its unprocessed form, and renders
 CC the virus noninfectious. The protease is therefore useful for assaying
 CC pharmaceutical agents for control of HCV, as compounds which inhibit
 CC protease activity sufficiently will also inhibit viral infectivity. An
 CC inactive non-cleaving protease can be used to screen for inhibitors.
 CC Recombinant expression systems can be utilised to prepare recombinant HCV
 CC which can be used to produce monoclonal antibodies. The present sequence
 CC was isolated in the course of the invention
 XX
 SQ Sequence 281 BP; 41 A; 89 C; 92 G; 59 T; 0 U; 0 Other;
 Query Match 2.7%; Score 56; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 292 TGCACCTTGGCGCTCTCGGACCTTTACTGCTCAGGAGGACGCCGATGTCATTCC 347
 DB 4 TGCACCTTGGCGCTCTCGGACCTTTACTGCTCAGGAGGACGCCGATGTCATTCC 59
 RESULT 21
 ID ACD44791 standard; DNA; 281 BP.
 AC ACD44791;
 XX
 DT 09-SEP-2003 (first entry)
 XX
 DE Hepatitis C virus (HCV) protease clone C8h DNA.
 XX
 KW Hepatitis C virus; HCV; protease; protease inhibition; viral infection;
 KW Gene; ds.
 XX
 OS Hepatitis C virus.
 XX
 FN US2003027317-A1.
 XX
 XX 06-FEB-2003.
 XX
 PF 18-JUN-2001; 2001US-00884456.
 XX
 PR 04-APR-1990; 90US-00505433.
 PR 04-APR-1991; 91US-00680296.
 PR 06-DEC-1994; 94US-00350884.
 PR 12-MAY-1995; 95US-00440348.
 PR 06-SEP-1996; 96US-00709177.
 PR 19-FEB-1999; 99US-00253230.
 XX
 XX (HOUG/) HOUGHTON M.
 PA (CHOO/) CHOO Q.
 PA (KUOG/) KUO G.
 XX
 FI Houghton M, Choo Q, Kuo G;
 XX
 DR WPI: 2003-492037/58.
 DR P-PSDB; ABC27015.
 XX
 PT New compositions comprising a hepatitis C virus (HCV) protease
 PT polynucleotide, useful for assaying pharmaceutical agents for controlling
 PT HCV, and as compounds which inhibit the protease activity and viral
 PT infectivity.
 XX

PS Example 3; Fig 4; 41pp; English.
 XX
 CC The invention describes a composition comprising a polynucleotide which
 CC encodes only the hepatitis C virus (HCV) protease or an active HCV
 CC protease analogue. The protease is useful for assaying pharmaceutical
 CC agents for controlling HCV, and as compounds which inhibit the protease
 CC activity sufficiently will also inhibit viral infectivity. This sequence
 CC encodes hepatitis C virus (HCV) protease
 XX
 SQ Sequence 281 BP; 41 A; 89 C; 92 G; 59 T; 0 U; 0 Other;
 Query Match 2.7%; Score 56; DB 8; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 292 TGCACCTTGGCGCTCTCGGACCTTTACTGCTCAGGAGGACGCCGATGTCATTCC 347
 DB 4 TGCACCTTGGCGCTCTCGGACCTTTACTGCTCAGGAGGACGCCGATGTCATTCC 59
 RESULT 22
 ID ADA07864 standard; cDNA; 281 BP.
 XX
 AC ADA07864;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Hepatitis C virus cDNA C8h encoding an NS3 protease fragment.
 XX
 KW ss; HCV; virucide; NS3 protease; serine protease; hSOD;
 KW superoxide dismutase; yeast a-factor; interleukin-28; ubiquitin;
 KW beta-galactosidase; beta-lactamase; horseradish peroxidase;
 KW glucose oxidase; urease; HCV infection.
 XX
 OS Hepatitis C virus.
 XX
 PN US2003064499-A1.
 XX
 PD 03-APR-2003.
 XX
 PF 18-JUN-2001; 2001US-00884455.
 XX
 PR 04-APR-1990; 90US-00505433.
 PR 04-APR-1991; 91US-00680296.
 PR 06-DEC-1994; 94US-00350884.
 PR 12-MAY-1995; 95US-00440348.
 PR 06-SEP-1996; 96US-00709177.
 PR 18-FEB-1999; 99US-00253675.
 XX
 XX (HOUG/) HOUGHTON M.
 PA (CHOO/) CHOO Q.
 PA (KUOG/) KUO G.
 XX
 FI Houghton M, Choo Q, Kuo G;
 XX
 DR WPI: 2003-540789/51.
 DR P-PSDB; ADA07865.
 XX
 PT A composition for assaying and designing antiviral agents specific for
 PT Hepatitis C virus (HCV) comprises a purified proteolytic polypeptide from
 PT HCV or a polynucleotide which encodes HCV protease.
 XX
 PS Example 3; Fig 4; 40pp; English.
 XX
 CC The invention relates to a composition comprising a purified proteolytic
 CC polypeptide derived from Hepatitis C virus (HCV) or a polynucleotide
 CC which encodes only the HCV protease or an active HCV protease analogue,
 CC or which encodes a fusion protein comprising HCV protease or HCV protease
 CC analogue, and a fusion partner. Also included are a fusion protein
 CC comprising a fusion partner fused to a proteolytic polypeptide derived
 CC from HCV, a method for assaying compounds for activity against HCV
 CC (comprising providing an active HCV protease, contacting the protease

CC with a compound capable of inhibiting serine protease activity and
CC measuring inhibition of the proteolytic activity of the HCV protease) and
CC an expression vector for producing HCV protease or HCV protease analogues
CC in a host cell (comprising a polynucleotide encoding HCV protease or an
CC HCV protease analogue, transcriptional and translational regulatory
CC sequences functional in the host cell operably linked to the HCV protease
CC -encoding polynucleotide and a selectable marker). The fusion partner is
CC selected from hSOD (human superoxide dismutase), yeast a-factor,
CC interleukin (IL)-2S, ubiquitin, beta-galactosidase, beta-lactamase,
CC horseradish peroxidase, glucose oxidase and urease. The composition is
CC useful in assaying and designing antiviral agents specific for HCV. The
CC method is used in identifying antiviral agents effective for treating
CC HCV. The present sequence is a cDNA encoding an HCV NS3 protease or
CC fragment.

XX SQ Sequence 281 BP; 41 A; 89 C; 92 G; 59 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGACGCGCATGTCATCC 347
Db 4 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGACGCGCATGTCATCC 59

RESULT 23

AAAN90317
ID AAAN90317 standard; DNA; 282 BP.

XX AC AAAN90317;

DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)

XX Hepatitis C virus (HCV) cDNA in clone 8h.

XX Hepatitis C virus; cDNA; clone 8h; clone 33c; probe; vaccine.

XX Pan troglodytes.

XX Key Location/Qualifiers
FH CDS 3..281
FT /*tag= a

FT misc_feature 212..283
FT /*tag= b

XX GB2212511-A.

XX 26-JUL-1989.

XX 18-NOV-1988; 88GB-00027024.

XX 18-NOV-1987; 87US-00122714.

XX 30-DEC-1987; 87US-00139886.

XX 26-FEB-1988; 88US-00161072.

XX 26-OCT-1988; 88US-00263584.

XX (CHIR) CHIRON CORP.

XX Houghton M, Choo QL, Kuo G;

XX WPI; 1989-215054/30.

XX P-PSDB; AAP90148.

XX Hepatitis C virus gene - used for prodn. of polynucleotide probes
XX polypeptide(s) and antibodies for diagnosis, prevention and treatment of
XX infection.

XX Disclosure; Fig 16; 30pp; English.

XX The sequence shows hepatitis C virus (HCV) cDNA in clone 8h. The cDNA
XX encodes antigens which react with antibodies in patients with non-A non-B

CC hepatitis (NANBH). The cDNA can be used to design probes, or to
CC synthesise polypeptides, which are used to diagnose HCV-induced NANBH, to
CC raise antibodies for immunoassay or treatment, or to produce vaccines.
CC The misc. feature indicates overlap with clone 33c. See also AAP90148,
CC AAN90303-15, and N903018-36. (Updated on 25-MAR-2003 to correct PD
CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
CC 2003 to correct PA field.)

XX SQ Sequence 282 BP; 41 A; 89 C; 92 G; 60 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGACGCGCATGTCATCC 347
Db 6 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGACGCGCATGTCATCC 61

RESULT 24

AAQ80170
ID AAQ80170 standard; DNA; 282 BP.

XX AC AAQ80170;

DT 25-MAR-2003 (revised)
DT 17-AUG-1995 (first entry)

XX Hepatitis C virus (HCV) protease clone C8h DNA.

XX Hepatitis C virus protease; HCV; clone C8h; viral infectivity inhibition;
XX ds.

XX Hepatitis C virus.

XX Key Location/Qualifiers
FH mat_peptide 1..280
FT /*tag= a

XX US5371017-A.

XX 06-DEC-1994.

XX 04-APR-1991; 91US-00680296.

XX 04-APR-1990; 90US-00505433.

XX (CHIR) CHIRON CORP.

XX Houghton M, Choo Q, Kuo G;

XX WPI; 1995-021889/03.

XX P-PSDB; AAR68542.

XX DNA encoding hepatitis C virus protease - used to produce large amts. of
XX the protease and to develop prods. for inhibition of viral infectivity.

XX Example 3; Fig 4; 69pp; English.

XX AAQ80170 encodes AAR68542 hepatitis C virus (HCV) protease clone C8h,
XX using recombinant expression systems large amounts of protease can be
XX produced. The HCV protease can be used in the production of Abs. It can
XX also be used for assaying agents which inhibit protease activity, to
XX identify compounds which inhibit viral infectivity. (Updated on 25-MAR-
XX 2003 to correct PF field.)

XX SQ Sequence 282 BP; 41 A; 89 C; 92 G; 59 T; 0 U; 1 Other;

Query Match 2.7%; Score 56; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGACGCGCATGTCATCC 347

Db 5 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACCGCGATGTCATTCC 60

RESULT 25
 AAN92087
 ID AAN92087 standard; DNA; 283 BP.
 AC AAN92087;
 XX
 DT 25-MAR-2003 (revised)
 DT 02-MAR-1990 (first entry)
 XX
 XX Sequence of the hepatitis C virus (HCV) cDNA insert in clone 8h.
 DE Hepatitis C virus; HCV; non-A, non-B hepatitis; NANBH.
 KW Hepatitis C virus.
 XX
 OS Hepatitis C virus.
 XX
 FH Key Location/Qualifiers
 FT CDS 3..281
 FT misc_feature /*tag= a
 FT 212..283
 FT /*tag= b
 XX
 PN EP318216-A.
 XX
 PD 31-MAY-1989.
 XX
 XX 18-NOV-1988; 98EP-00310922.
 XX
 PR 18-NOV-1987; 87US-00122714.
 PR 30-DEC-1987; 87US-00139886.
 PR 26-FEB-1988; 88US-00161072.
 PR 06-MAY-1988; 88US-00191263.
 PR 26-OCT-1988; 88US-00263584.
 PR 14-NOV-1988; 88US-00271450.
 XX
 PA (CHIR) CHIRON CORP.
 PA (CHIR) CHIRON CORP.
 XX
 PI Houghton M, Choo Q, Kuo G;
 XX
 WPI; 1989-159274/22.
 DR P-PSDB; AAP92031.
 XX
 PT Purified hepatitis C virus - and associated nucleic acids and
 PT polypeptide(s).
 XX
 PS Claim 3; Fig 16; 139pp; English.
 XX

It is a double-stranded nucleotide sequence of the hepatitis C virus (HCV) cDNA insert in clone 8h. It is not necessarily physically derived from HCV cDNA and may be generated in any manner. Tag b = the region of overlap with clone 33c. It was isolated using a hybridization probe based on clone 33c. It contains one continuous open reading frame (tag a). The ORF encodes an epitope. AAN92087 could be used as a source of oligomeric DNA hybridisation probes to detect the presence of HCV nucleic acids in samples. The polypeptide(s) it encodes could be used as immunosay reagents and vaccines and to generate antibodies useful in diagnosis and passive immunotherapy for HCV infection/non-A, non-B hepatitis. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 283 BP; 41 A; 90 C; 92 G; 60 T; 0 U; 0 Other;
 Query Match 2.7%; Score 56; DB 1; Length 283;
 Best Local Similarity 100.0%; Pred. No. 1e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACCGCGATGTCATTCC 347
 Db 6 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACCGCGATGTCATTCC 61

RESULT 26
 AAQ14297
 ID AAQ14297 standard; DNA; 368 BP.
 AC AAQ14297;
 XX
 DT 25-MAR-2003 (revised)
 DT 14-JAN-1992 (first entry)
 XX
 XX Hepatitis C Virus protease clone C20c.
 DE
 XX NANBH; non-A, non-B hepatitis; liver disease; fusion protein; ds.
 KW
 XX Hepatitis C virus.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..368
 FT /*tag= a
 FT /*note= "partial CDS only"

XX WO9115575-A.
 XX 17-OCT-1991.
 XX
 XX 04-APR-1990; 90US-00505433.
 XX
 XX 04-APR-1990; 90US-00505433.
 XX
 XX (CHIR) CHIRON CORP.
 XX
 PI Houghton M, Choo Q, Kuo G;
 XX
 WPI; 1991-325218/44.
 DR P-PSDB; AAR14539.
 XX
 XX New purified protease - derived from hepatitis C virus, for assay, and
 XX designing anti-HCV agents.
 XX
 PS Example 3; Fig 2; 74pp; English.
 XX

XX Clone C20c was isolated from a HCV cDNA library (ATCC 40394) using probe C20c (see AAQ14308). It was digested with EcoRI and SmaI to give a 260bp fragment. This fragment, along with a fragment from clone C7f (see AAQ14300), was cloned into the EcoRI site of pBR322 and transformed into E.coli. A fragment from this recombinant vector was eventually used to construct a vector which encodes amino acids 1-151 of human Superoxide dismutase fused to amino acids 946-1630 of HCV protease. The vector (cf1SODp600) was transformed into E.coli D1210 cells and deposited as ATCC 68275. (Updated on 25-MAR-2003 to correct PA field.)
 XX
 XX Sequence 368 BP; 70 A; 114 C; 108 G; 76 T; 0 U; 0 Other;
 Query Match 2.7%; Score 56; DB 2; Length 368;
 Best Local Similarity 100.0%; Pred. No. 1e-17;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACCGCGATGTCATTCC 347
 Db 220 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCACGAGGCACCGCGATGTCATTCC 275

RESULT 27
 AAQ14359
 ID AAQ14359 standard; DNA; 368 BP.
 AC AAQ14359;
 XX
 DT 16-JAN-1992 (first entry)
 XX
 XX Clone C20c encoding HCV protease gene.
 DE
 XX

XX Hepatitis C virus; HCV; human superoxide dismutase; SOD; ds.

XX Hepatitis C virus.

XX WO9115596-A.

XX 17-OCT-1991.

XX 04-APR-1990; 90US-00505434.

XX 04-APR-1990; 90US-00505434.

XX (PROT-) PROTOS INC.

XX Rosenberg S;

XX WPI; 1991-325236/44.

XX P-PSDB; AAR14350.

XX Method for assaying pharmaceutical cpds. - for determining anti-Hepatitis C Virus activity, using binding affinity.

XX Example 3; Fig 2; 68pp; English.

XX The DNA from the clone was used to prepare a hSOD:HCV protease fusion construct. The truncated protease analogue expressed by the resulting vector is proteolytically inactive and can be used to assay a wide range of pharmaceutical agents for controlling HCV. Those agents which inhibit the protease activity sufficiently will also inhibit viral infectivity. See also AAQ14358-Q14365

XX Sequence 368 BP; 70 A; 114 C; 108 G; 76 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 2; Length 368;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 347

Db 220 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 275

RESULT 28

AAQ80168

ID AAQ80168 standard; DNA; 368 BP.

XX AAQ80168;

XX 25-MAR-2003 (revised)

DT 17-AUG-1995 (first entry)

XX Hepatitis C virus (HCV) protease clone C20c DNA.

XX Hepatitis C virus protease; HCV; clone C20c;

XX viral infectivity inhibition; ds.

XX Hepatitis C virus.

XX Key Location/Qualifiers

FT mat_peptide 1..366

FT /*tag= a

XX US5371017-A.

XX 06-DEC-1994.

XX 04-APR-1991; 91US-00680296.

XX 04-APR-1990; 90US-00505433.

XX (CHIR) CHIRON CORP.

XX Houghton M, Choo Q, Kuo G;

XX

DR WPI; 1995-021889/03.

DR P-PSDB; AAR68540.

XX

PT DNA encoding hepatitis C virus protease - used to produce large amts. of the protease and to develop prods. for inhibition of viral infectivity.

XX

PS Example 3; Fig 2; 69pp; English.

XX

CC AAQ80168 encodes AAR68540 hepatitis C virus (HCV) protease clone C20c, using recombinant expression systems large amounts of protease can be produced. The HCV protease can be used in the production of Abs. It can also be used for assaying agents which inhibit protease activity, to identify compounds which inhibit viral infectivity. (Updated on 25-MAR-2003 to correct Pf field.)

XX

SQ Sequence 368 BP; 70 A; 114 C; 108 G; 76 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 2; Length 368;

Best Local Similarity 100.0%; Pred. No. 1e-17;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 347

Db 220 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 275

RESULT 29

AAT59254

ID AAT59254 standard; DNA; 368 BP.

XX

AC AAT59254;

XX

DT 17-OCT-2003 (revised)

DT 25-MAR-2003 (revised)

DT 03-APR-1997 (first entry)

XX

DE HCV protease clone C20c.

XX

KW HCV; NS3; non-structural domain 3; protease; polyprotein; inhibitor;

KW screen, processing; infection; treatment; probe; hepatitis C virus; ss.

XX

OS Hepatitis C virus; Virus.

XX

PN US5585258-A.

XX

PD 17-DEC-1996.

XX

PF 06-DEC-1994; 94US-00350884.

XX

PR 04-APR-1990; 90US-00505433.

XX

PR 04-APR-1991; 91US-00680296.

XX

PA (CHIR) CHIRON CORP.

XX

PI Choo Q, Kuo G, Houghton M;

XX

DR WPI; 1997-051175/05.

XX

DR P-PSDB; AAW01690.

XX

PT Compns. contg. hepatitis C virus NS3 domain protease and related fusion proteins - useful for screening specific inhibitors, potential antiviral agents, prepn. of antibodies and for cleaving specific poly:peptide(s).

XX

PS Example 3; Col 63-64; 68pp; English.

XX

CC Compns. comprising the hepatitis C virus (HCV) NS3 domain protease or its active truncation analogues are claimed. Also new are fusion proteins comprising the protease (or analogues) and, e.g. human superoxide (SOD) or ubiquitin. The protease is essential for polyprotein processing, and thus infectivity, in HCV. The compns. are used to screen for specific inhibitors (possibly useful as antiviral agents), to generate specific antibodies and to cleave specific polypeptides. HCV cDNA clones (AAT59250


```
XX AC ACD44789;
XX AC
XX DT 09-SEP-2003 (first entry)
XX DE Hepatitis C virus (HCV) protease clone C20c DNA.
XX DE
XX DE Hepatitis C virus; HCV; protease; protease inhibition; viral infection;
XX KW gene; ds.
XX OS Hepatitis C virus.
XX OS
XX PN US2003027317-A1.
XX PD 06-FEB-2003.
XX PF 18-JUN-2001; 2001US-00884456.
XX PR 04-APR-1990; 90US-00505433.
XX PR 04-APR-1991; 91US-00680296.
XX PR 06-DEC-1994; 94US-00350884.
XX PR 12-MAY-1995; 95US-00440548.
XX PR 06-SEP-1996; 96US-00709177.
XX PR 19-FEB-1999; 99US-00253230.
XX PR
XX (HOUG/) HOUGHTON M.
XX PA (CHOO/) CHOO Q.
XX PA (KUOG/) KUO G.
XX PI Houghton M, Choo Q, Kuo G;
XX PS
XX DR WPI; 2003-492037/58.
XX DR P-PSDB; ABO27013.
XX
XX New compositions comprising a hepatitis C virus (HCV) protease
XX PT polynucleotide, useful for assaying pharmaceutical agents for controlling
XX PT HCV, and as compounds which inhibit the protease activity and viral
XX PT infectivity.
XX
XX Example 3; Fig 2; 4lpp; English.
XX
XX The invention describes a composition comprising a polynucleotide which
XX CC encodes only the hepatitis C virus (HCV) protease or an active HCV
XX CC protease analogue. The protease is useful for assaying pharmaceutical
XX CC agents for controlling HCV, and as compounds which inhibit the protease
XX CC activity sufficiently will also inhibit viral infectivity. This sequence
XX CC encodes hepatitis C virus (HCV) protease
XX
XX Sequence 368 BP; 70 A; 114 C; 108 G; 76 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 56; DB 8; Length 368;
XX Best Local Similarity 100.0%; Pred. No. 1e-17;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTGCACGAGGACGCCGATGTCATTC 347
XX 220 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTGCACGAGGACGCCGATGTCATTC 275
XX
XX RESULT 33
XX ADA07860
XX ID ADA07860 standard; cDNA; 368 BP.
XX AC ADA07860;
XX
XX 06-NOV-2003 (first entry)
XX
XX Hepatitis C virus cDNA C20c encoding an NS3 protease fragment.
XX
XX ss; HCV; virucide; NS3 protease; serine protease; hSOD;
XX KW superoxide dismutase; yeast a-factor; interleukin-2S; ubiquitin;
XX KW beta-galactosidase; beta-lactamase; horseradish peroxidase;
XX KW glucose oxidase; urease; HCV infection.
```

```
XX OS Hepatitis C virus.
XX OS
XX PN US2003064499-A1.
XX PD 03-APR-2003.
XX PF 18-JUN-2001; 2001US-00884455.
XX PR 04-APR-1990; 90US-00505433.
XX PR 04-APR-1991; 91US-00680296.
XX PR 06-DEC-1994; 94US-00350884.
XX PR 12-MAY-1995; 95US-00440548.
XX PR 06-SEP-1996; 96US-00709177.
XX PR 18-FEB-1999; 99US-00253675.
XX PR
XX (HOUG/) HOUGHTON M.
XX PA (CHOO/) CHOO Q.
XX PA (KUOG/) KUO G.
XX PI Houghton M, Choo Q, Kuo G;
XX DR WPI; 2003-540789/51.
XX DR P-PSDB; ADA07861.
XX
XX A composition for assaying and designing antiviral agents specific for
XX PT Hepatitis C virus (HCV) comprises a purified proteolytic polypeptide from
XX PT HCV or a polynucleotide which encodes HCV protease.
XX
XX Example 3; Fig 2; 40pp; English.
XX
XX The invention relates to a composition comprising a purified proteolytic
XX CC polypeptide derived from Hepatitis C virus (HCV) or a polynucleotide
XX CC which encodes only the HCV protease or an active HCV protease analogue,
XX CC or which encodes a fusion protein comprising HCV protease or HCV protease
XX CC analogue, and a fusion partner. Also included are a fusion protein
XX CC comprising a fusion partner fused to a proteolytic polypeptide derived
XX CC from HCV, a method for assaying compounds for activity against HCV
XX CC (comprising providing an active HCV protease, contacting the protease
XX CC with a compound capable of inhibiting serine protease activity and
XX CC measuring inhibition of the proteolytic activity of the HCV protease) and
XX CC an expression vector for producing HCV protease or HCV protease analogues
XX CC in a host cell (comprising a polynucleotide encoding HCV protease or an
XX CC HCV protease analogue, transcriptional and translational regulatory
XX CC sequences functional in the host cell operably linked to the HCV protease
XX CC -encoding polynucleotide and a selectable marker). The fusion partner is
XX CC selected from hSOD (human superoxide dismutase), yeast a-factor,
XX CC interleukin (IL)-2S, ubiquitin, beta-galactosidase, beta-lactamase,
XX CC horseradish peroxidase, glucose oxidase and urease. The composition is
XX CC useful in assaying and designing antiviral agents specific for HCV. The
XX CC method is used in identifying antiviral agents effective for treating
XX CC HCV. The present sequence is a cDNA encoding an HCV NS3 protease or
XX CC fragment.
```

```
XX SQ Sequence 368 BP; 70 A; 114 C; 108 G; 76 T; 0 U; 0 Other;
XX
XX Query Match 2.7%; Score 56; DB 8; Length 368;
XX Best Local Similarity 100.0%; Pred. No. 1e-17;
XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTGCACGAGGACGCCGATGTCATTC 347
Db 220 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTGCACGAGGACGCCGATGTCATTC 275
```

```
RESULT 34
ABX15706
ID ABX15706 standard; DNA; 612 BP.
XX
XX AC ABX15706;
XX
XX 28-MAR-2003 (first entry)
XX
```

DE Anti-viral synthetic prototoxophore associated DNA sequence.
XX Hepatitis C; ds; viral prototoxophore; anti-viral; tumour; virus;
KW infection; antitumour; toxophore; human immunodeficiency virus;
KW HIV infection; herpes simplex virus; HSV; rhinovirus; NS3 protease.
XX Unidentified.
XX WO200287500-A2.
PN 07-NOV-2002.
XX 26-APR-2002; 2002WO-US013223.
XX 27-APR-2001; 2001US-0286893P.
PR (NEWB-) NEWBIOTICS INC.
XX Catheers BE, Neuteboom STC, Shepard HW;
XX WPI; 2003-167102/16.
XX Novel synthetic viral prototoxophore for treating viral infections, has
FT toxin moiety incorporated into substrate domain specific for viral
PT enzyme, bound and modified by viral enzyme to get converted into
XX toxophore.
XX Example 1; Page 62; 66pp; English.
XX This invention relates to a novel synthetic viral prototoxophore
CC comprising a toxin moiety operatively incorporated into a substrate
CC domain specific for a viral enzyme. This prototoxophore may be bound and
CC modified by the viral enzyme thus converting it to a toxophore. Also
CC disclosed in the invention is a method for enhancing the anti-viral
CC effect of an antiviral agent, this method comprises contacting a cell,
CC infected with a virus or is susceptible to infection, with a
CC prototoxophore. The invention further comprises an assay to identify anti
CC -viral agents, comprising contacting an infected cell with a candidate
CC agent and comparing the ability of the agent to inhibit the growth or
CC infectivity of the virus in the cell. The prototoxophores of the
CC invention may have virucide or antitumour activity. The prototoxophores
CC of the invention may be useful for reducing or inhibiting viral
CC infectivity, by contacting a cell (e.g. lymphocyte, nerve cell,
CC connective tissue cell, muscle cell or hepatocyte) which is infected with
CC a virus or is susceptible to infection with a virus, with an effective
CC amount of the prototoxophore. The cells are cell lines adapted to long
CC term continuous culture or isolated from a subject. The prototoxophore is
CC also useful for ameliorating the severity of a viral infection in a
CC subject, where the virus is selected from human immunodeficiency virus
CC (HIV), herpes simplex virus (HSV), rhinovirus and hepatitis virus, by
CC administering an effective amount of the prototoxophore to the subject.
CC The prototoxophores of the invention are also useful for treating
CC tumours. The present sequence represents an antiviral prototoxophore
CC associated DNA sequence, this sequence is described as a recombinant
CC NS3/NS4 fusion protein in example 1 of the invention although it is
CC clearly not a protein sequence
XX
XX Sequence 612 BP; 120 A; 171 C; 191 G; 130 T; 0 U; 0 Other;
SQ
Query Match 2.7%; Score 56; DB 8; Length 612;
Best Local Similarity 100.0%; Pred. No. 1e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 292 TGCACCTTCGGCTCTCTCGGACCTTTACCTGCTACGAGGACCGCGATGTCATTC 347
Db 349 TGCACCTTCGGCTCTCTCGGACCTTTACCTGCTACGAGGACCGCGATGTCATTC 404
RESULT 35
AAQ14304
ID AAQ14304 standard; DNA; 1947 BP.
XX AAQ14304;
AC

XX 25-MAR-2003 (revised)
DT 14-JAN-1992 (first entry)
XX Vector cf1SODp600 sequence encoding hSOD-HCV protease fusion protein.
DE NANBH; non-A, non-B hepatitis; liver disease;
KW human superoxide dismutase leader sequence; ds.
XX Hepatitis C virus.
OS
XX Key Location/Qualifiers
FH sig_peptide 1..465
FT /tag= a
FT /label= hSOD leader
FT mat_peptide 466..1947
FT /tag= b
FT /product= "HCV protease"
XX WO9115575-A.
PN 17-OCT-1991.
XX 04-APR-1990; 90US-00505433.
XX 04-APR-1990; 90US-00505433.
XX (CHIR) CHIRON CORP.
XX Houghton M, Choo Q, Kuo G;
XX WPI; 1991-325218/44.
DR P-PSDB; AAR14546.
XX New purified protease - derived from hepatitis C virus, for assay, and
PT designing anti-HCV agents.
FT
XX Example 4; Fig 10; 74pp; English.
PS cf1SODp600 was transformed into E.coli D1210 cells and deposited as ATCC
CC 68275. The full-length HCV protease coding sequence was constructed from
CC a number of different clones (see AAQ14297-Q14303). (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
XX Sequence 1947 BP; 427 A; 539 C; 566 G; 415 T; 0 U; 0 Other;
SQ
Query Match 2.7%; Score 56; DB 2; Length 1947;
Best Local Similarity 100.0%; Pred. No. 9.7e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 292 TGCACCTTCGGCTCTCTCGGACCTTTACCTGCTACGAGGACCGCGATGTCATTC 347
Db 1000 TGCACCTTCGGCTCTCTCGGACCTTTACCTGCTACGAGGACCGCGATGTCATTC 1055
RESULT 36
ABK15344
ID ABK15344 standard; DNA; 2058 BP.
XX
XX ABK15344;
AC
XX 08-MAY-2002 (first entry)
DT
DE Hepatitis C virus NS3/4a conformational epitope gene sequence.
XX Hepatitis C virus; HCV; NS3/4a conformational epitope; seroconversion;
KW immunoassay solid support; multiple epitope fusion antigen; MEPA;
KW non-structural protein; gene; ds.
XX
XX Hepatitis C virus.
OS
XX Key Location/Qualifiers
FH CDS 1..2058
FT


```
FT FT /*tag= a
FT FT /partial
FT FT /product= "HCV NS3/4a conformational epitope"
FT FT /note= "This sequence lacks a stop codon"
XX PN WO200196870-A2.
XX XX 20-DEC-2001.
XX XX 14-JUN-2001; 2001WO-US019156.
XX XX 15-JUN-2000; 2000US-0212082P.
XX XX 02-APR-2001; 2001US-0280811P.
XX XX 02-APR-2001; 2001US-0280867P.
XX XX (CHIR ) CHIRON CORP.
XX XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
XX XX Medina-Selby A;
XX XX WPI; 2002-090228/12.
XX XX P-PSDB; AAU76377.
XX XX
XX XX Immunoassay solid support, useful for detecting hepatitis C virus
XX XX infection in biological sample, comprises HCV NS3/4a conformational
XX XX epitope and multiple epitope fusion antigen bound to the support.
XX XX Disclosure; Fig 3; 92pp; English.
XX XX
XX XX The present invention relates to a new immunoassay solid support
XX XX consisting essentially of at least one hepatitis C virus (HCV) NS3/4a
XX XX conformational epitope and a multiple epitope fusion antigen (MEFA),
XX XX bound to the support. The NS3/4a conformational epitope and/or MEFA
XX XX reacts specifically with anti-HCV antibodies present in a biological
XX XX sample from an HCV-infected individual. The immunoassay of the invention
XX XX is useful for detecting hepatitis C virus infection in a biological
XX XX sample. The method of the invention provides a sensitive, accurate
XX XX diagnostic and prognostic tool to provide adequate patient care and to
XX XX prevent transmission of HCV by blood and by blood products, or by
XX XX personal contact. Use of NS3/4a conformational epitope in combination
XX XX with MEFA, provides a sensitive and reliable method for detecting early
XX XX HCV seroconversion. Use of MEFA has the added advantages of decreasing
XX XX masking problems, improving sensitivity in detecting antibodies by
XX XX allowing a greater number of epitopes on a unit surface area of
XX XX substrate, and improving substrate. Detection accuracy is increased and
XX XX the incidence of false results is reduced because of the identification
XX XX and the use of highly immunogenic HCV antigens which are present during
XX XX the early stages of HCV seroconversion. The present nucleic acid sequence
XX XX encodes the non-structural protein NS3/4a conformational epitope of the
XX XX invention
XX XX
XX XX Sequence 2058 BP; 419 A; 633 C; 581 G; 425 T; 0 U; 0 Other;
XX XX
XX XX Query Match 2.7%; Score 56; DB 6; Length 2058;
XX XX Best Local Similarity 100.0%; Pred. No. 9.7e-18;
XX XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTACGAGGACGCGCATGTCATTC 347
XX XX |||||
XX XX 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTACGAGGACGCGCATGTCATTC 347
XX XX
XX XX RESULT 37
XX XX AAD29795
XX XX AAD29795 standard; DNA; 2058 BP.
XX XX
XX XX AAD29795;
XX XX
XX XX 17-MAY-2002 (first entry)
XX XX
XX XX HCV-1 NS3/4a mutant conformational antigen encoding DNA.
XX XX
XX XX Hepatitis C virus; NS3/4a antigen; HCV infection; mutant; ds.
XX XX
```

```
XX XX Hepatitis C virus type 1.
XX OS Synthetic.
XX XX
XX FH Key Location/Qualifiers
XX FT 1..686
XX FT /*tag= a
XX FT /product= "HCV-1 NS3/4a conformational antigen"
XX FT /note= "CDS does not include stop codon"
XX FT /partial
XX XX
XX PN WO200196875-A2.
XX XX 20-DEC-2001.
XX XX 14-JUN-2001; 2001WO-US019369.
XX XX 15-JUN-2000; 2000US-0212082P.
XX XX 02-APR-2001; 2001US-0280811P.
XX XX 02-APR-2001; 2001US-0280867P.
XX XX (CHIR ) CHIRON CORP.
XX XX
XX XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;
XX XX Medina-Selby A;
XX XX WPI; 2002-179522/23.
XX XX P-PSDB; AAE18689.
XX XX
XX XX Immunoassay solid support useful for detecting hepatitis C virus
XX XX infection in a biological sample, comprises at least one of HCV anti-core
XX XX antibody and HCV NS3/4a epitope, bound to the support.
XX XX Example 2; Fig 4; 87pp; English.
XX XX
XX XX The present invention relates to hepatitis C virus (HCV) core antigen and
XX XX NS (nonstructural) 3/4a antibody combination assay that can detect both
XX XX HCV antigens and antibodies present in a sample using a single solid
XX XX matrix as well as immunoassay solid supports for use in the assay. The
XX XX solid support is useful for detecting HCV infection in a biological
XX XX sample. The present sequence is a DNA encoding HCV-1 NS3/4a mutant
XX XX conformational antigen. This sequence is used in the exemplification of
XX XX the invention
XX XX
XX XX Sequence 2058 BP; 419 A; 634 C; 580 G; 425 T; 0 U; 0 Other;
XX XX
XX XX Query Match 2.7%; Score 56; DB 6; Length 2058;
XX XX Best Local Similarity 100.0%; Pred. No. 9.7e-18;
XX XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX XX
XX XX 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTACGAGGACGCGCATGTCATTC 347
XX XX |||||
XX XX 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTACGAGGACGCGCATGTCATTC 347
XX XX
XX XX RESULT 38
XX XX ABX14410
XX XX ID ABX14410 standard; DNA; 2058 BP.
XX XX
XX XX ABX14410;
XX XX
XX XX 06-MAR-2003 (first entry)
XX XX
XX XX DNA encoding HCV-1 NS3/4a conformational antigen.
XX XX
XX XX Immunoassay solid support; Hepatitis C virus type-1; HCV-1;
XX XX NS3/4a conformational epitope; multiple epitope fusion antigen; MEFA;
XX XX anti-HCV antibody; NS3/4a conformational antigen; HCV infection; mutant;
XX XX gene; ds.
XX XX
XX XX Hepatitis C virus type 1.
XX OS Synthetic.
XX XX
```

KW Key Location/Qualifiers
 FT 1..2058
 FT /*tag= a
 FT /partial
 FT /product= "NS3/4a conformational antigen"
 FT /note= "This sequence lacks a stop codon"

XX US2002146685-A1.

XX 10-OCT-2002.

XX 14-JUN-2001; 2001US-00881654.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIE//) CHIEN D. Y.

XX (AFCA//) ARCANGEL P.

XX (TAND//) TANDESKE L.

XX (GEOR//) GEORGE-NASCIMENTO C.

XX (COIT//) COIT D.

XX (MEDI//) MEDINA-SELBY A.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI; 2003-147573/14.

XX P-PSDB; ABG72261.

XX Immunoassay solid support for detecting Hepatitis C Virus infection in biological samples, comprises Hepatitis C Virus conformational epitope and multiple epitope fusion antigen.

XX Disclosure; Fig 3A-3D; 45pp; English.

XX The present invention relates to immunoassays comprising Hepatitis C Virus (HCV) NS3/4a conformational epitope and multiple epitope fusion antigen (MEFA), bound to a solid support. The NS3/4a epitope and/or the multiple epitope fusion antigen react with anti-HCV antibodies present in a biological sample from an HCV-infected individual. The immunoassays and methods of the invention are useful for detecting HCV infection in a biological sample. The inventive immunoassay solid support provides a sensitive and reliable method for detecting early HCV seroconversion. The assays can detect HCV infection caused by any six known genotypes of HCV. The use of the multiple epitope fusion proteins decreases masking problems, improves sensitivity in detecting antibodies by allowing a greater number of epitopes on a unit area of substrate, and improves selectivity. The present sequence encodes HCV type 1 (HCV-1) NS3/4a conformational antigen, a mutant of the HCV-1 NS3/4a polypeptide

XX Sequence 2058 BP; 419 A; 633 C; 581 G; 425 T; 0 U; 0 Other;

XX Query Match 2.7%; Score 56; DB 7; Length 2058;

XX Best Local Similarity 100.0%; Pred. No. 9.7e-18;

XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTACCTGGTACAGGACCGCCGATGTCATCC 347

DB 292 TGCACCTTGGCGCTCCTCGGACCTTACCTGGTACAGGACCGCCGATGTCATCC 347

RESULT 39

ADCO6768

ID ADC06768 standard; DNA; 2058 BP.

XX AC ADC06768;

XX 18-DEC-2003 (first entry)

XX HCV mutant conformational NS3/4a epitope DNA.

XX immunoassay solid support; HCV; NS3/4a; non-structural;

KW non-A, non-B hepatitis; NANB; conformational epitope; mutant; ds; gene.
 XX Synthetic.
 OS Hepatitis C virus.
 XX Key Location/Qualifiers
 FT 1..2058
 FT /*tag= a
 FT /partial
 FT /product= "HCV mutant conformational NS3/4a epitope
 FT protein T403P/S404I"
 FT /note= "No stop codon"

XX US2002192639-A1.

XX 19-DEC-2002.

XX 14-JUN-2001; 2001US-00881239.

XX 15-JUN-2000; 2000US-0212082P.

XX 02-APR-2001; 2001US-0280811P.

XX 02-APR-2001; 2001US-0280867P.

XX (CHIE//) CHIEN D. Y.

XX (ARCA//) ARCANGEL P.

XX (TAND//) TANDESKE L.

XX (GEOR//) GEORGE-NASCIMENTO C.

XX (COIT//) COIT D.

XX (MEDI//) MEDINA-SELBY A.

XX Chien DY, Arcangel P, Tandeske L, George-Nascimento C, Coit D;

XX Medina-Selby A;

XX WPI; 2003-644509/61.

XX P-PSDB; ABC06767.

XX Immunoassay solid support for detecting hepatitis C virus infection in biological samples, comprises a hepatitis C virus anti-core antibody and an isolated hepatitis C virus NS3/4a epitope bound HCV anti-core antibody.

XX Example 2; Fig 4; 40pp; English.

XX The invention relates to a novel immunoassay solid support comprising at least one hepatitis C virus (HCV) anti-core antibody and at least one isolated HCV NS3/4a (non-structural protein 3/4a) epitope bound thereto. The system of the invention may be useful for detecting HCV infection in a biological sample and for treating or detecting non-A, non-B hepatitis (NANB hepatitis). The current sequence is that of the HCV mutant conformational NS3/4a epitope DNA of the invention.

XX Sequence 2058 BP; 419 A; 634 C; 580 G; 425 T; 0 U; 0 Other;

XX Query Match 2.7%; Score 56; DB 9; Length 2058;

XX Best Local Similarity 100.0%; Pred. No. 9.7e-18;

XX Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTACCTGGTACAGGACCGCCGATGTCATCC 347

DB 292 TGCACCTTGGCGCTCCTCGGACCTTACCTGGTACAGGACCGCCGATGTCATCC 347

RESULT 40

AAQ14296

ID AAQ14296 standard; cDNA; 2064 BP.

XX AC AAQ14296;

XX 25-MAR-2003 (revised)

XX 14-JAN-1992 (first entry)

XX Hepatitis C Virus protease.

XX Example 1; Col 53-60; 68pp; English.
 PS This sequence encodes part of the hepatitis C virus (HCV) polyprotein
 CC which contains the NS3 domain protease. Compsns. comprising the HCV
 CC protease or its active truncation analogues are claimed. Also new are
 CC fusion proteins comprising the protease (or analogues) and, e.g. human
 CC superoxide or ubiquitin. The protease is essential for polyprotein
 CC processing, and thus infectivity, in HCV. The compsns. are used to screen
 CC for specific inhibitors (possibly useful as antiviral agents), to
 CC generate specific antibodies and to cleave specific polypeptides.
 CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 17-OCT-2003 to
 CC standardise OS field)
 XX Sequence 2064 BP; 413 A; 641 C; 583 G; 427 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 2; Length 2064;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 292 TGCACCTTGGCGCTCCTCGACCTTTACCTGTCACGAGGCACGCCGATGTCATCC 347
 Db 541 TGCACCTTGGCGCTCCTCGACCTTTACCTGTCACGAGGCACGCCGATGTCATCC 596

RESULT 43
 AAV04985
 ID AAV04985 standard; DNA; 2064 BP.
 XX AC AAV04985;
 XX DT 27-AUG-2003 (revised)
 XX DT 07-MAY-1998 (first entry)
 XX DE Nucleotide sequence encoding Hepatitis C virus (HCV) protease.
 XX Protease; HCV; NS3 domain; human superoxide dismutase; fusion protein;
 XX ubiquitin; assay; activity; anti-HCV; ss.

XX Hepatitis C virus.
 XX Key Location/Qualifiers
 XX CDS 7..2064
 XX /*tag= a
 XX /note= "no ATG start or STOP codons given"
 XX US5712145-A.
 XX 27-JAN-1998.

XX PF 06-SEP-1996; 96US-00709173.
 XX PR 04-APR-1990; 90US-00505433.
 XX PR 04-APR-1991; 91US-00680296.
 XX PR 06-DEC-1994; 94US-00350884.
 XX PR 12-MAY-1995; 95US-00440548.

XX (CHIR) CHIRON CORP.

XX Choo Q, Kuo G, Houghton M;

XX WPI; 1998-119986/11.
 XX P-PSDB; AAW46389.

XX Recombinant hepatitis C virus protease - useful in screening drugs for
 XX activity against hepatitis C virus.

XX Disclosure; Fig 1A-F; 68pp; English.

XX The present sequence encodes a Hepatitis C virus (HCV) protease. The
 CC protein is encoded by sequences within the NS3 domain. The protease is
 CC believed to cleave itself from the genomic polyprotein. In the absence of
 CC protease activity, the HCV polyprotein should remain in its unprocessed

CC form, and thus render the virus non-infectious. Inhibitors of protease
 CC activity should therefore also inhibit viral infectivity. The protease is
 CC used for assaying compounds for activity against HCV. (Updated on 27-AUG-
 CC 2003 to correct OS field.)

XX SQ Sequence 2064 BP; 413 A; 641 C; 583 G; 427 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 2; Length 2064;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGACCTTTACCTGTCACGAGGCACGCCGATGTCATCC 347
 Db 541 TGCACCTTGGCGCTCCTCGACCTTTACCTGTCACGAGGCACGCCGATGTCATCC 596

RESULT 44
 AAX26390
 ID AAX26390 standard; DNA; 2064 BP.

XX AC AAX26390;

XX DT 26-MAY-1999 (first entry)

XX DE DNA encoding the HCV protease of the invention.

XX HCV NS3 protease; truncation analog; HCV control; protease activity;
 XX viral infectivity; inactive non-cleaving protease; ss.

XX Hepatitis C virus.

XX Key Location/Qualifiers

XX CDS 7..2064
 XX /*tag= a
 XX /note= "no termination codon"

XX US5885799-A.

XX 23-MAR-1999.

XX PF 06-SEP-1996; 96US-00709177.

XX PR 04-APR-1990; 90US-00505433.

XX PR 04-APR-1991; 91US-00680296.

XX PR 06-DEC-1994; 94US-00350884.

XX PR 12-MAY-1995; 95US-00440548.

XX (CHIR) CHIRON CORP.

XX Choo Q, Kuo G, Houghton M;

XX WPI; 1999-228536/19.

XX P-PSDB; AAW97601.

XX Preparation of new Hepatitis C Virus NS3 protease - useful for screening
 XX for compounds which inhibit HCV infectivity.

XX Example 4; Fig 1; 71pp; English.

XX The specification describes a method for making a purified Hepatitis C
 CC virus (HCV) NS3 protease or active truncation analog. If the HCV protease
 CC N-terminal cleavage signal is excluded (so that self-cleavage is
 CC prevented), the HCV protease remains in its unprocessed form, and renders
 CC the virus noninfectious. The protease is therefore useful for assaying
 CC pharmaceutical agents for control of HCV, as compounds which inhibit
 CC protease activity sufficiently will also inhibit viral infectivity. An
 CC inactive non-cleaving protease can be used to screen for inhibitors.
 CC Recombinant expression systems can be utilised to prepare recombinant HCV
 CC which can be used to produce monoclonal antibodies. The present sequence
 CC appears in the specification

XX Sequence 2064 BP; 413 A; 641 C; 583 G; 427 T; 0 U; 0 Other;

Query Match 2.7%; Score 56; DB 2; Length 2064;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347
 Db 541 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 596

RESULT 45
 ACD44788
 ID ACD44788 standard; DNA; 2064 BP.
 XX AC ACD44788;
 XX DT 09-SEP-2003 (first entry)
 XX DE Hepatitis C virus (HCV) protease DNA.
 XX KW Hepatitis C virus; HCV; protease; protease inhibition; viral infection;
 XX KW Gene; ds.
 XX OS Hepatitis C virus.
 XX PN US2003027317-A1.
 XX PD 06-FEB-2003.
 XX PF 18-JUN-2001; 2001US-00884456.
 XX PR 04-APR-1990; 90US-00505433.
 XX PR 04-APR-1991; 91US-00680296.
 XX PR 06-DEC-1994; 94US-00350884.
 XX PR 12-MAY-1995; 95US-00440548.
 XX PR 06-SEP-1996; 96US-00709177.
 XX PR 18-FEB-1999; 99US-00253230.
 XX PA (HOUG/) HOUGHTON M.
 XX PA (CHOO/) CHOO Q.
 XX PA (KUOG/) KUO G.
 XX PI Houghton M, Choo Q, Kuo G;
 XX DR WPI; 2003-492037/58.
 XX DR P-PSDB; ABO27012.
 XX PT New compositions comprising a hepatitis C virus (HCV) protease
 XX PT polynucleotide, useful for assaying pharmaceutical agents for controlling
 XX PT HCV, and as compounds which inhibit the protease activity and viral
 XX PT infectivity.
 XX PS Example 2; Fig 1; 41pp; English.
 XX CC The invention describes a composition comprising a polynucleotide which
 XX CC encodes only the hepatitis C virus (HCV) protease or an active HCV
 XX CC protease analogue. The protease is useful for assaying pharmaceutical
 XX CC agents for controlling HCV, and as compounds which inhibit the protease
 XX CC activity sufficiently will also inhibit viral infectivity. This sequence
 XX CC encodes hepatitis C virus (HCV) protease
 XX Sequence 2064 BP; 413 A; 641 C; 583 G; 427 T; 0 U; 0 Other;
 Query Match 2.7%; Score 56; DB 8; Length 2064;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347
 Db 541 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 596

RESULT 46
 ADA07858

ID ADA07858 standard; cDNA; 2064 BP.
 XX AC ADA07858;
 XX DT 06-NOV-2003 (first entry)
 XX DE Hepatitis C virus cDNA encoding the NS3 protease.
 XX KW ss; gene; HCV; virucide; NS3 protease; serine protease; hSOD;
 XX KW superoxide dismutase; yeast a-factor; interleukin-2S; ubiquitin;
 XX KW beta-galactosidase; beta-lactamase; horseradish peroxidase;
 XX KW glucose oxidase; urease; HCV infection.
 XX OS Hepatitis C virus.
 XX PN US2003064499-A1.
 XX PD 03-APR-2003.
 XX PF 18-JUN-2001; 2001US-00884455.
 XX PR 04-APR-1990; 90US-00505433.
 XX PR 04-APR-1991; 91US-00680296.
 XX PR 06-DEC-1994; 94US-00350884.
 XX PR 12-MAY-1995; 95US-00440548.
 XX PR 06-SEP-1996; 96US-00709177.
 XX PR 18-FEB-1999; 99US-00253675.
 XX PA (HOUG/) HOUGHTON M.
 XX PA (CHOO/) CHOO Q.
 XX PA (KUOG/) KUO G.
 XX PI Houghton M, Choo Q, Kuo G;
 XX DR WPI; 2003-540789/51.
 XX DR P-PSDB; ADA07859.
 XX PT A composition for assaying and designing antiviral agents specific for
 XX PT Hepatitis C virus (HCV) comprises a purified proteolytic polypeptide from
 XX PT HCV or a polynucleotide which encodes HCV protease.
 XX PS Example 2; Fig 1; 40pp; English.
 XX CC The invention relates to a composition comprising a purified proteolytic
 XX CC polypeptide derived from Hepatitis C virus (HCV) or a polynucleotide
 XX CC which encodes only the HCV protease or an active HCV protease analogue,
 XX CC or which encodes a fusion protein comprising HCV protease or HCV protease
 XX CC analogue, and a fusion partner. Also included are a fusion protein
 XX CC comprising a fusion partner fused to a proteolytic polypeptide derived
 XX CC from HCV, a method for assaying compounds for activity against HCV
 XX CC (comprising providing an active HCV protease, contacting the protease
 XX CC with a compound capable of inhibiting serine protease activity and
 XX CC measuring inhibition of the proteolytic activity of the HCV protease) and
 XX CC an expression vector for producing HCV protease or HCV protease analogues
 XX CC in a host cell (comprising a polynucleotide encoding HCV protease or an
 XX CC HCV protease analogue, transcriptional and translational regulatory
 XX CC sequences functional in the host cell operably linked to the HCV protease
 XX CC -encoding polynucleotide and a selectable marker). The fusion partner is
 XX CC selected from hSOD (human superoxide dismutase), yeast a-factor,
 XX CC interleukin (IL)-2S, ubiquitin, beta-galactosidase, beta-lactamase,
 XX CC horseradish peroxidase, glucose oxidase and urease. The composition is
 XX CC useful in assaying and designing antiviral agents specific for HCV. The
 XX CC method is used in identifying antiviral agents effective for treating
 XX CC HCV. The present sequence is the full length cDNA encoding the HCV NS3
 XX CC protease.
 XX Sequence 2064 BP; 413 A; 641 C; 583 G; 427 T; 0 U; 0 Other;
 Query Match 2.7%; Score 56; DB 8; Length 2064;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGGTCACGAGGACGCCGATGTCATTC 347

Db 541 TGCACCTTGGGCTCTCGGACCTTTACTGTCACGAGCGACCGGATGTCATTCC 596
|||||
RESULT 47
ABX15705
ID ABX15705 standard; cDNA; 2073 BP.
XX AC ABX15705;
XX DT 28-MAR-2003 (first entry)
XX DE cDNA sequence encoding hepatitis C virus NS3 and NS4A protease genes.
XX KW Hepatitis C; ss; viral prototoxophore; anti-viral; tumour; NS4A; virus;
XX KW infection; antitumour; toxophore; human immunodeficiency virus;
XX KW HIV infection; herpes simplex virus; HSV; rhinovirus; NS3 protease.
XX OS Hepatitis C virus.
XX OS Synthetic.
XX PN WO200287500-A2.
XX PD 07-NOV-2002.
XX PF 26-APR-2002; 2002WO-US013223.
XX PR 27-APR-2001; 2001US-0286893P.
XX PA (NEWB-) NEWBIOTICS INC.
XX PI Cathers BE, Neuteboom STC, Shepard HM;
XX WPI; 2003-167102/16.
XX Novel synthetic viral prototoxophore for treating viral infections, has
XX toxin moiety incorporated into substrate domain specific for viral
XX enzyme, bound and modified by viral enzyme to get converted into
XX toxophore.
XX Example 1; Page 62; 66pp; English.
XX This invention relates to a novel synthetic viral prototoxophore
XX comprising a toxin moiety operatively incorporated into a substrate
XX domain specific for a viral enzyme. This prototoxophore may be bound and
XX modified by the viral enzyme thus converting it to a toxophore. Also
XX disclosed in the invention is a method for enhancing the anti-viral
XX effect of an antiviral agent, this method comprises contacting a cell,
XX infected with a virus or is susceptible to infection, with a
XX prototoxophore. The invention further comprises an assay to identify anti
XX -viral agents, comprising contacting an infected cell with a candidate
XX agent and comparing the ability of the agent to inhibit the growth or
XX infectivity of the virus in the cell. The prototoxophores of the
XX invention may have virucide or antitumour activity. The prototoxophores
XX of the invention may be useful for reducing or inhibiting viral
XX infectivity, by contacting a cell (e.g. lymphocyte, nerve cell,
XX connective tissue cell, muscle cell or hepatocyte) which is infected with
XX a virus or is susceptible to infection with a virus, with an effective
XX amount of the prototoxophore. The cells are cell lines adapted to long
XX term continuous culture or isolated from a subject. The prototoxophore is
XX also useful for ameliorating the severity of a viral infection in a
XX subject, where the virus is selected from human immunodeficiency virus
XX (HIV), herpes simplex virus (HSV), rhinovirus and hepatitis virus, by
XX administering an effective amount of the prototoxophore to the subject.
XX The prototoxophores of the invention are also useful for treating
XX tumours. The present sequence represents a cDNA sequence encoding the
XX Hepatitis C virus NS3 and NS4A protease genes for use in an assay to
XX measure the conversion of a prototoxophore of the invention to an
XX activated toxophore in cells transfected with this gene
XX SQ Sequence 2073 BP; 423 A; 635 C; 581 G; 434 T; 0 U; 0 Other;
Query Match 2.7%; Score 56; DB 8; Length 2073;
Best Local Similarity 100.0%; Pred. No. 9.7e-18; Length 2073;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 9.7e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTTGGGCTCTCGGACCTTTACTGTCACGAGCGACCGGATGTCATTCC 347
|||||
Db 298 TGCACCTTGGGCTCTCGGACCTTTACTGTCACGAGCGACCGGATGTCATTCC 353
|||||
RESULT 48
AAQ14358
ID AAQ14358 standard; DNA; 2523 BP.
XX AC AAQ14358;
XX DT 16-JAN-1992 (first entry)
XX DE HCV protease gene::hsod leader fusion in cf1SODp600.
XX KW Hepatitis C virus; HCV; human superoxide dismutase; SOD; ss.
XX OS Hepatitis C virus.
XX FH Key Location/Qualifiers
FT Signal_peptide 1..465 /*tag= a
FT /*note= "hsod leader sequence"
FT Misc_RNA 466..2523 /*tag= b
FT /*product= "AAS 946-1630 of HCV"
XX PN WO9115596-A.
XX PD 17-OCT-1991.
XX PF 04-APR-1990; 90US-00505434.
XX PR 04-APR-1990; 90US-00505434.
XX PA (PROT-) PROTOS INC.
XX PI Rosenberg S;
XX WPI; 1991-325236/44.
XX P-PSDB; AAR14349.
XX Method for assaying pharmaceutical cpds. - for determining anti-Hepatitis
XX C Virus activity, using binding affinity.
XX Example 4; Fig 10; 68pp; English.
XX The vector cf1SODp600 contains a full-length HCV protease coding sequence
XX fused to a functional hsod leader. The truncated protease analogue
XX expressed by the vector is proteolytically inactive and can be used to
XX assay a wide range of pharmaceutical agents for controlling HCV. Those
XX agents which inhibit the protease activity sufficiently will also inhibit
XX viral infectivity. See also AAQ14359-Q14365
XX SQ Sequence 2523 BP; 546 A; 722 C; 718 G; 537 T; 0 U; 0 Other;
Query Match 2.7%; Score 56; DB 2; Length 2523;
Best Local Similarity 100.0%; Pred. No. 9.7e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTTGGGCTCTCGGACCTTTACTGTCACGAGCGACCGGATGTCATTCC 347
|||||
Db 1000 TGCACCTTGGGCTCTCGGACCTTTACTGTCACGAGCGACCGGATGTCATTCC 1055
|||||
RESULT 49
AAQ80175
ID AAQ80175 standard; DNA; 2523 BP.
XX AC AAQ80175;
Query Match 2.7%; Score 56; DB 8; Length 2073;
Best Local Similarity 100.0%; Pred. No. 9.7e-18; Length 2073;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

same as 5-885, 789A

XX 25-MAR-2003 (revised)
 DT 17-AUG-1995 (first entry)
 XX HCV protease/hSOD fusion protein expression vector cflSODp600.
 DE Hepatitis C virus protease/hSOD fusion protein; HCV;
 XX expression vector cflSODp600; viral infectivity inhibition; ds.
 KW Hepatitis C virus.
 XX
 OS
 XX Key Location/Qualifiers
 FH CDS 1..2523
 FT /*tag= a
 FT sig_peptide 1..465
 FT /*tag= b
 FT /*label= hSOD leader
 FT
 XX
 XX US5371017-A.
 XX 06-DEC-1994.
 XX 04-APR-1991; 91US-00680296.
 XX 04-APR-1990; 90US-00505433.
 XX (CHIR) CHIRON CORP.
 XX Houghton M, Choo Q, Kuo G;
 XX WPI; 1995-021889/03.
 DR P-PSDB; AAR68547.
 XX
 XX DNA encoding hepatitis C virus protease - used to produce large amts. of
 PT the protease and to develop prods. for inhibition of viral infectivity.
 PT
 PS Claim 10; Fig 10; 69pp; English.
 XX
 XX AAQ80175 (which encodes AAR68547) describes the sequence of the hepatitis
 CC C virus (HCV) protease/hSOD fusion protein E. coli expression vector,
 CC cflSODp600. Other claimed HCV protease fusion partners are yeast alpha-
 CC factor, IL-28, ubiquitin, beta-galactosidase, beta-lactamase, horseradish
 CC peroxidase, glucose oxidase and urease. The HCV protease fusion proteins
 CC can be used in the production of Abs. They can also be used for assaying
 CC agents which inhibit protease activity, to identify compounds which
 CC inhibit viral infectivity. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 2523 BP; 544 A; 724 C; 718 G; 537 T; 0 U; 0 Other;
 SQ
 Query Match 2.7%; Score 56; DB 2; Length 2523;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTCC 347
 DB 1000 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTCC 1055
 RESULT 50
 AAT59261
 ID AAT59261 standard; DNA; 2523 BP.
 XX
 AC AAT59261;
 XX
 DT 17-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 03-APR-1997 (first entry)
 XX
 DE cflSODp600 encoding hSOD-HCV fusion protein.
 XX
 XX HCV; NS3; non-structural domain 3; protease; polyprotein; inhibitor;
 KW screen; processing; infection; treatment; probe; hepatitis C virus; ss.
 XX

OS Hepatitis C virus; Virus.
 OS Homo sapiens.
 OS Chimeric.
 XX
 PN US5585258-A.
 XX 17-DEC-1996.
 XX 06-DEC-1994; 94US-00350884.
 PR 04-APR-1990; 90US-00505433.
 PR 04-APR-1991; 91US-00680296.
 PA (CHIR) CHIRON CORP.
 XX Choo Q, Kuo G, Houghton M;
 XX WPI; 1997-051175/05.
 DR P-PSDB; AAW01701.
 XX
 XX Compsn. contg. hepatitis C virus NS3 domain protease and related fusion
 PT proteins - useful for screening specific inhibitors, potential antiviral
 PT agents, prepn. of antibodies and for cleaving specific polypeptide(s).
 XX
 PS Example 4; Col 77-84; 68pp; English.
 XX
 XX Compsns. comprising the hepatitis C virus (HCV) NS3 domain protease or
 CC its active truncation analogues are claimed. Also new are fusion proteins
 CC comprising the protease (or analogues) and, e.g. human superoxide (SOD)
 CC or ubiquitin. The protease is essential for polypeptide processing, and
 CC thus infectivity, in HCV. The comsns. are used to screen for specific
 CC inhibitors (possibly useful as antiviral agents), to generate specific
 CC antibodies and to cleave specific polypeptides. HCV cDNA clones (AAT59250
 CC - 56 encoding AAW01686-92 resp.) were isolated from HCV genomic library
 CC using probes AAT59244-49. The clones were used in the preparation of full
 CC length SOD-protease fusion proteins. The present sequence is that of
 CC vector cflSODp600 which contains a full-length HCV protease coding
 CC sequence fused to a functional hSOD leader. The resulting vector encodes
 CC amino acids 1-151 of hSOD, and amino acids 946-1630 of HCV (corresponding
 CC to 1-686 of AAW01693). (Updated on 25-MAR-2003 to correct PF field.)
 XX
 XX Sequence 2523 BP; 545 A; 722 C; 719 G; 537 T; 0 U; 0 Other;
 SQ
 Query Match 2.7%; Score 56; DB 2; Length 2523;
 Best Local Similarity 100.0%; Pred. No. 9.7e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTCC 347
 DB 1000 TGCACCTTGGCGCTCCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTCC 1055
 Search completed: August 19, 2004, 06:43:15
 Job time : 791 secs

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2004, 06:14:30 ; Search time 173 Seconds

Title: US-09-930-591-1
Perfect score: 2061
Sequence: 1 atggcgctatcacggccta.....atgaatggaagagtgctga 2061

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 35

Total number of hits satisfying chosen parameters: 116

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA.*

1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*

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3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*

4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*

5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seq.*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	62	3.0	943	2	US-08-483-695-6
2	62	3.0	943	2	US-07-965-285-6
3	62	3.0	943	2	US-08-487-231-6
4	62	3.0	943	3	US-09-201-912-6
5	58	2.8	382	4	US-08-867-611-56
6	58	2.8	382	4	US-09-690-359-56
7	58	2.8	1414	3	US-08-867-611-51
8	58	2.8	1414	4	US-09-690-359-51
9	58	2.8	1420	3	US-08-867-611-57
10	58	2.8	1420	4	US-09-690-359-57
11	56	2.7	281	1	US-08-350-884-75
12	56	2.7	281	1	US-08-440-548-75
13	56	2.7	281	1	US-08-709-173-75
14	56	2.7	281	1	US-08-709-173-75
15	56	2.7	283	3	US-08-444-818-33
16	56	2.7	368	1	US-08-350-884-71
17	56	2.7	368	1	US-08-440-548-71
18	56	2.7	368	1	US-08-709-173-71
19	56	2.7	368	2	US-08-709-173-71
20	56	2.7	2058	4	US-09-881-654-1
21	56	2.7	2058	4	US-09-881-654-1
22	56	2.7	2064	1	US-08-350-884-69
23	56	2.7	2064	1	US-08-440-548-69
24	56	2.7	2064	1	US-08-709-173-69
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26	56	2.7	2523	1	US-08-350-884-85
27	56	2.7	2523	1	US-08-440-548-85
28	56	2.7	2523	1	US-08-709-173-85
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30	56	2.7	5360	3	US-08-444-818-53
31	56	2.7	5785	3	US-08-444-818-65
32	56	2.7	7310	3	US-08-444-818-74
33	56	2.7	8316	3	US-08-444-818-88
34	56	2.7	8987	3	US-08-444-818-137
35	56	2.7	9185	3	US-08-444-818-122
36	56	2.7	9185	3	US-08-444-818-123
37	56	2.7	9379	3	US-08-444-818-176
38	56	2.7	9379	3	US-08-388-874-1
39	56	2.7	9379	4	US-09-916-359-1
40	56	2.7	9401	1	US-07-910-760-9
41	56	2.7	9401	1	US-08-440-519-9
42	56	2.7	9401	4	US-08-440-549-9
43	56	2.7	9401	4	US-08-823-895A-25
44	56	2.7	9401	5	PCT-US91-02225-9
45	53	2.6	9416	4	US-08-823-895A-26
46	53	2.6	9416	4	US-10-104-966-13
47	53	2.6	9599	3	US-09-014-416-2
48	53	2.6	9599	3	US-09-014-416-6
49	53	2.6	9646	3	US-08-811-566-1
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52	53	2.5	885	3	US-08-511-759B-1
53	52	2.5	885	3	US-09-592-197-1
54	52	2.5	885	3	US-09-592-197-1
55	52	2.5	885	4	US-08-892-704-1
56	50	2.4	373	4	US-08-469-260A-669
57	50	2.4	373	4	US-08-488-446-669
58	50	2.4	373	4	US-08-467-344A-669
59	50	2.4	1251	3	US-08-867-611-19
60	50	2.4	1251	4	US-09-690-359-19
61	50	2.4	1251	5	PCT-US92-06965A-24
62	44	2.1	492	3	US-08-444-818-25
63	44	2.1	800	3	US-08-444-818-31
64	44	2.1	816	1	US-08-350-884-83
65	44	2.1	816	1	US-08-440-548-83
66	44	2.1	816	1	US-08-709-173-83
67	44	2.1	816	2	US-08-709-173-83
68	44	2.1	2219	3	US-08-444-818-147
69	44	2.1	2499	4	US-09-881-239-4
70	44	2.1	2579	3	US-08-444-818-29
71	44	2.1	3075	1	US-07-910-760-11
72	44	2.1	3075	1	US-08-440-519-11
73	44	2.1	3075	4	US-08-440-549-11
74	44	2.1	3297	4	US-09-881-654-3
75	44	2.1	9401	2	US-08-432-693-1
76	44	2.1	9416	3	US-08-811-566-19
77	44	2.1	9416	4	US-09-034-756-19
78	44	2.1	9472	4	US-08-150-204E-96
79	43	2.1	347	3	US-08-444-818-35
80	41	2.0	268	3	US-08-444-818-21
81	41	2.0	307	3	US-08-444-818-143
82	41	2.0	308	1	US-08-350-884-79
83	41	2.0	308	1	US-08-440-548-79
84	41	2.0	308	1	US-08-709-173-79
85	41	2.0	308	2	US-08-709-173-79
86	41	2.0	477	1	US-07-853-985A-7
87	41	2.0	477	1	US-07-681-703B-7
88	41	2.0	477	1	US-08-184-236-7
89	41	2.0	477	2	US-08-407-410B-7
90	41	2.0	477	2	US-08-485-500-7
91	41	2.0	477	5	PCT-US91-02370-7
92	41	2.0	477	5	PCT-US94-04174-7
93	41	2.0	480	3	US-08-444-818-17
94	41	2.0	495	1	US-08-350-884-81
95	41	2.0	495	1	US-08-440-548-81
96	41	2.0	495	1	US-08-709-173-81
97	41	2.0	495	2	US-08-709-173-81
98	41	2.0	558	1	US-07-853-985A-9
99	41	2.0	558	1	US-07-681-703B-9
100	41	2.0	558	1	US-08-184-236-9

Sequence 9, Appli
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Sequence 9, Appli
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Sequence 19, Appli
Sequence 19, Appli
Sequence 4, Appli
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Sequence 6, Appli
Sequence 1, Appli
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Sequence 1, Appli

101 41 2.0 558 2 US-08-407-410B-9
102 41 2.0 558 2 US-08-485-500-9
103 41 2.0 558 5 PCT-US91-02370-9
104 41 2.0 558 5 PCT-US94-04174-9
105 41 2.0 943 2 US-08-483-695-43
106 41 2.0 943 2 US-07-965-285-43
107 41 2.0 943 2 US-08-487-231-43
108 41 2.0 943 3 US-09-201-912-43
109 41 2.0 1382 3 US-08-444-818-19
110 41 2.0 1932 3 US-09-128-314-1
111 41 2.0 7659 3 US-09-128-314-4
112 41 2.0 8157 3 US-09-128-314-3
113 35 1.7 267 1 US-08-685-764-6
114 35 1.7 7475 2 US-08-971-036-1
115 35 1.7 7475 3 US-09-096-570-1
116 35 1.7 7475 4 US-09-265-617B-1

ALIGNMENTS

RESULT 1
US-08-483-695-6
; Sequence 6, Application US/08483695
; Patent No. 5866139
; GENERAL INFORMATION:
; APPLICANT: Brechot, Christian
; APPLICANT: Kremsdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,695
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,285
; FILING DATE: 18-MAR-1993
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; DESCRIPTION: cdna to genomic RNA
US-08-483-695-6

Query Match 3.0%; Score 62; DB 2; Length 943;

Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1915 GCGCGCTTCTGGCTGCTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGCTTCTGGCTGCTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 689

QY 1975 GG 1976
Db 690 GG 691

RESULT 2
US-07-965-285-6
; Sequence 6, Application US/07965285
; Patent No. 5879904
; GENERAL INFORMATION:
; APPLICANT: Brechot, Christian
; APPLICANT: Kremsdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91-06-882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; DESCRIPTION: cdna to genomic RNA
US-07-965-285-6

Query Match 3.0%; Score 62; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1915 GCGCGCTTCTGGCTGCTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGCTTCTGGCTGCTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 689

QY 1975 GG 1976
Db 690 GG 691

RESULT 3
US-08-487-231-6
; Sequence 6, Application US/08487231
; Patent No. 5919454
; GENERAL INFORMATION:
; APPLICANT: Brechot, Christian
; APPLICANT: Kremsdorf, Dina
; APPLICANT: Porchon, Colette
; TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
; TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
; TITLE OF INVENTION: Applications
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,231
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,285
; FILING DATE: 18-MAR-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 06 882
; FILING DATE: 06-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 05286-0001-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 943 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other
; DESCRIPTION: cdna to genomic RNA
US-08-487-231-6
Query Match 3.0%; Score 62; DB 2; Length 943;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1915 GCGCGGCTTCGCTGCTTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGGCTTCGCTGCTTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 689
QY 1975 GG 1976
Db 690 GG 691
RESULT 4
US-09-201-912-6
; Sequence 6, Application US/09201912
; Patent No. 6210962
; GENERAL INFORMATION:
; APPLICANT: Brechot, Christian

APPLICANT: Kremsdorf, Dina
APPLICANT: Porchon, Colette
TITLE OF INVENTION: Nucleotide and Peptide Sequences of a
TITLE OF INVENTION: Hepatitis C Virus Isolate, Diagnostic and Therapeutic
TITLE OF INVENTION: Applications
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,912
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/965,285
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 05286-0001-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 943 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other
DESCRIPTION: cdna to genomic RNA
US-09-201-912-6
Query Match 3.0%; Score 62; DB 3; Length 943;
Best Local Similarity 100.0%; Pred. No. 8.8e-22;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1915 GCGCGGCTTCGCTGCTTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 1974
Db 630 GCGCGGCTTCGCTGCTTTGGCGCGCTATTGCTATCCACAGGCTGCGTGCATAGTA 689
QY 1975 GG 1976
Db 690 GG 691
RESULT 5
US-08-867-611-56
; Sequence 56, Application US/08867611
; Patent No. 6122189
; GENERAL INFORMATION:
; APPLICANT: DEVARE, SUSHIL G
; APPLICANT: DESAI, SURESH M
; APPLICANT: CASEY, JAMES M
; APPLICANT: DAILEY, STEPHEN H
; APPLICANT: DAWSON, GEORGE J
; APPLICANT: GUTIERREZ, ROBIN A
; APPLICANT: LESNIEWSKI, RICHARD R
; APPLICANT: STEWART, JAMES L
; APPLICANT: RUPPRECHT, KEVIN R
; TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
; TITLE OF INVENTION: ANTIGENS
; NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/867,611
FILING DATE: 02-JUN-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/646,757
FILING DATE:
APPLICATION NUMBER: US/08/179,896
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834 US.P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-867-611-56

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Query Match          2.8%; Score 58; DB 3; Length 382;
Best Local Similarity 100.0%; Pred.No. 1e-19;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1291 ACGTGTGTACCCAGACAGTCGACTTCAGCCCTTGACCTACCTCACCATTGAGCAA 1348
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Db 33 ACGTGTGTACCCAGACAGTCGACTTCAGCCCTTGACCTACCTCACCATTGAGCAA 90

RESULT 6
US-09-690-359-56
; Sequence 56, Application US/09690359
; Patent No. 6593083
; GENERAL INFORMATION:
; APPLICANT: DEVARE, SUSHIL G
; DESAI, SURESH M
; CASEY, JAMES M
; DAILY, STEPHEN H
; DAWSON, GEORGE J
; GUTIERREZ, ROBIN A
; LESNIEWSKI, RICHARD
;

STEWART, JAMES L
RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT
ANTIGENS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/690,359
FILING DATE: 17-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/867,611
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: US/08/646,757
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/179,896
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 382 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-690-359-56

Query Match 2.8%; Score 58; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1291 ACGTGTGCACCCAGACAGTCGACTTCAGCCTTGACCTACCTCACCATTGAGACAA 1348

Db 33 ACGTGTGCACCCAGACAGTCGACTTCAGCCTTGACCTACCTCACCATTGAGACAA 90

RESULT 7
US-C8-867-611-51
; Sequence 51, Application US/08867611
; Patent No. 6172189
; GENERAL INFORMATION:
; APPLICANT: DEVADE, SUSHIL G-
; APPLICANT: DESAI, SURESH M
; APPLICANT: CASEY, JAMES M
; APPLICANT: DAILEY, STEPHEN H

APPLICANT: DAWSON, GEORGE J
APPLICANT: GUTIERREZ, ROBIN A
APPLICANT: LESNIEWSKI, RICHARD R
APPLICANT: STEWART, JAMES L
APPLICANT: RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT ANTIGENS
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT ANTIGENS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM: disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/867,611
FILING DATE: 02-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,757
FILING DATE:
APPLICATION NUMBER: US/08/179,896
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-867-611-51

Query Match 2.8%; Score 58; DB 3; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9.9e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTACCTTACCATTTGAGACAA 1348
DB 22 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTACCTTACCATTTGAGACAA 79

RESULT 8
US-09-690-359-51
; Sequence 51, Application US/09690359
; Patent No. 6593083

GENERAL INFORMATION:
APPLICANT: DEVARE, SUSHIL G
APPLICANT: DESAI, SURESH M
CASEY, JAMES M
DAILEY, STEPHEN H
DAWSON, GEORGE J
GUTIERREZ, ROBIN A
LESNIEWSKI, RICHARD R
STEWART, JAMES L
RUPPRECHT, KEVIN R
TITLE OF INVENTION: HEPATITIS C ASSAY UTILIZING RECOMBINANT ANTIGENS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: ABBOTT LABORATORIES
STREET: ONE ABBOTT PARK ROAD, CHAD377/AP6D2
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/690,359
FILING DATE: 17-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/867,611
FILING DATE: 02-JUN-1997
APPLICATION NUMBER: US/08/646,757
FILING DATE: <Unknown>
APPLICATION NUMBER: US 07/572,822
FILING DATE: 24-AUG-1990
APPLICATION NUMBER: US 07/614,069
FILING DATE: 07-NOV-1990
APPLICATION NUMBER: US 07/748,561
FILING DATE: 21-AUG-1991
APPLICATION NUMBER: US 07/748,565
FILING DATE: 21-AUG-1991
APPLICATION NUMBER: US 07/748,566
FILING DATE: 21-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 4834.US.P6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-937-9556
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 1414 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-690-359-51

Query Match 2.8%; Score 58; DB 4; Length 1414;
Best Local Similarity 100.0%; Pred. No. 9.9e-20;
Matches 58; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1291 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTACCTTACCATTTGAGACAA 1348
DB 22 ACGTGTGTCACCCAGACAGTCGACTTCAGCCTTACCTTACCATTTGAGACAA 79

RESULT 9


```

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..279
US-08-709-173-75

Query Match      2.7%; Score 56; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 347
Db      4 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 59

RESULT 14
US-08-709-177-75
; Sequence 75, Application US/08709177
; Patent No. 5885799
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KOO, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,177
; FILING DATE: 06-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 75:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 base pairs
; TYPE: nucleic acid

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```

; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..279
US-08-709-177-75

Query Match      2.7%; Score 56; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 347
Db      4 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 59

RESULT 15
US-08-444-818-33
; Sequence 33, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 283 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..281
US-08-444-818-33

Query Match      2.7%; Score 56; DB 3; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 347
Db      6 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTCC 61

RESULT 16

```


US-08-350-884-71
; Sequence (71) Application US/08350884
; Patent No. 5595258

GENERAL INFORMATION:

APPLICANT: HOUGHTON, MICHAEL

APPLICANT: CHOO, QUI LIM

APPLICANT: KUI, GEORGE

TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/350,884

FILING DATE: 06-DEC-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/680,296

FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: CIOTTI, THOMAS E.

REGISTRATION NUMBER: 21,013

REFERENCE/DOCKET NUMBER: 22300-20100.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 368 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..366

US-08-350-884-71

Query Match 2.7%; Score 56; DB 1; Length 368;

Best Local Similarity 100.0%; Pred. No. 1.1e-18;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATCC 347

Db 220 TGCACCTTGGGCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATCC 275

RESULT 17

US-08-440-548-71

; Sequence-71 Application US/08440548

; Patent No. 5597691

GENERAL INFORMATION:

APPLICANT: HOUGHTON, MICHAEL

APPLICANT: CHOO, QUI LIM

APPLICANT: KUI, GEORGE

TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,548
FILING DATE: 12-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 71:

SEQUENCE CHARACTERISTICS:

LENGTH: 368 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..366

US-08-440-548-71

Query Match 2.7%; Score 56; DB 1; Length 368;

Best Local Similarity 100.0%; Pred. No. 1.1e-18;

Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATCC 347

Db 220 TGCACCTTGGGCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATCC 275

RESULT 18

US-08-709-125-71

; Sequence (71) Application US/08709173

; Patent No. 5712145

GENERAL INFORMATION:

APPLICANT: HOUGHTON, MICHAEL

APPLICANT: CHOO, QUI LIM

APPLICANT: KUI, GEORGE

TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: California

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,173

FILING DATE: 06-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/680,296

FILING DATE: 04-APR-1991

ATTORNEY/AGENT INFORMATION:

NAME: CIOTTI, THOMAS E.

REGISTRATION NUMBER: 21,013

REFERENCE/DOCKET NUMBER: 22300-20100.20

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..366
US-08-709-173-71

Query Match 2.7%; Score 56; DB 1; Length 368;
Best Local Similarity 100.0%; Pred. No. 1.le-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGCTACGAGGACGCCGCGATGTCATTCC 347
Db 220 TGCACCTTGGCGCTCTCGGACCTTTACCTGCTACGAGGACGCCGCGATGTCATTCC 275

RESULT 19
US-08-709-177-71
Sequence 71 Application US/08709177
Patent No. 6630298
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
APPLICANT: KUO, GEORGE
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,177
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 368 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..366
US-08-709-177-71

Query Match 2.7%; Score 56; DB 2; Length 368;

Best Local Similarity 100.0%; Pred. No. 1.le-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGCTACGAGGACGCCGCGATGTCATTCC 347
Db 220 TGCACCTTGGCGCTCTCGGACCTTTACCTGCTACGAGGACGCCGCGATGTCATTCC 275

RESULT 20
US-09-881-239-2
Sequence 2 Application US/09881239
Patent No. 6630298
GENERAL INFORMATION:
APPLICANT: CHIEN, David Y.
APPLICANT: ARCANDEL, Phillip
APPLICANT: TANDESKE, Laura
APPLICANT: GEORGE-NASCIEMENTO, Carlos
APPLICANT: COIT, Doris
APPLICANT: MEDINA-SELBY, Angelica
TITLE OF INVENTION: HCV ANTIGEN/ANTIBODY COMBINATION ASSAY
FILE REFERENCE: 2302-16073 / PPI6073.003
CURRENT APPLICATION NUMBER: US/09/881,239
CURRENT FILING DATE: 2001-06-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2058
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: representative NS3/4a conformational antigen
NAME/KEY: CDS
LOCATION: (1)..(2058)
US-09-881-239-2

Query Match 2.7%; Score 56; DB 4; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1.le-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGCTACGAGGACGCCGCGATGTCATTCC 347
Db 292 TGCACCTTGGCGCTCTCGGACCTTTACCTGCTACGAGGACGCCGCGATGTCATTCC 347

RESULT 21
US-09-881-654-1
Sequence 1 Application US/09881654
Patent No. 6632601
GENERAL INFORMATION:
APPLICANT: CHIEN, David Y.
APPLICANT: ARCANDEL, Phillip
APPLICANT: TANDESKE, Laura
APPLICANT: GEORGE-NASCIEMENTO, Carlos
APPLICANT: COIT, Doris
APPLICANT: MEDINA-SELBY, Angelica
TITLE OF INVENTION: IMMUNOCASSAYS FOR ANTI-HCV ANTIBODIES
FILE REFERENCE: 2302-17039 / PPI7039.002
CURRENT APPLICATION NUMBER: US/09/881,654
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/212,082
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/280,811
PRIOR FILING DATE: 2001-04-02
PRIOR APPLICATION NUMBER: 60/280,867
PRIOR FILING DATE: 2001-04-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 2058
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: representative N33/4a conformational antigen
; NAME/KEY: CDS
; LOCATION: (1)..(2058)
US-09-881-654-1

Query Match 2.7%; Score 56; DB 4; Length 2058;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347
Db 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347

RESULT 22

US-08-350-884-69
; Sequence 69, Application US/08350884
; Patent No. 5585258
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUI, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08350,884
; FILING DATE: 06-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2064 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..2064
US-08-350-884-69

Query Match 2.7%; Score 56; DB 1; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347
Db 541 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 596

RESULT 23

US-08-350-884-69
; Sequence 69, Application US/08350884
; Patent No. 5585258
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUI, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08350,884
; FILING DATE: 06-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2064 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..2064
US-08-350-884-69

Query Match 2.7%; Score 56; DB 1; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347
Db 541 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 596

US-08-440-548-69
; Sequence 69, Application US/08440548
; Patent No. 5597691
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUI, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08440,548
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2064 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..2064
US-08-440-548-69

Query Match 2.7%; Score 56; DB 1; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347
Db 541 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 596

RESULT 24

US-08-709-173-69
; Sequence 69, Application US/08709173
; Patent No. 5712145
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUI, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08709,173
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2064 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..2064
US-08-709-173-69

Query Match 2.7%; Score 56; DB 1; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347
Db 541 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 596

RESULT 25

US-08-709-173-69
; Sequence 69, Application US/08709173
; Patent No. 5712145
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUI, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08709,173
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 69:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2064 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 7..2064
US-08-709-173-69

Query Match 2.7%; Score 56; DB 1; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 347
Db 541 TGCACCTTGGGCTCTCGGACCTTTACCTGGTACAGGACGCCGCGATGTCATTC 596

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,173
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2064
US-08-709-173-69

Query Match 2.7%; Score 56; DB 1; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACTGTCACGAGGACGCCGATGTCATTCC 347
DB 541 TGCACCTTGGCGCTCCTCGGACCTTTACTGTCACGAGGACGCCGATGTCATTCC 596

RESULT 25
US-08-709-173-69
Sequence 69, Application US/08709177
Patent No. 5885799
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,177
FILING DATE: 06-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2064 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 7..2064
US-08-709-177-69

Query Match 2.7%; Score 56; DB 2; Length 2064;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACTGTCACGAGGACGCCGATGTCATTCC 347
DB 541 TGCACCTTGGCGCTCCTCGGACCTTTACTGTCACGAGGACGCCGATGTCATTCC 596

RESULT 26
US-08-350-884-85
Sequence 85, Application US/08350884
Patent No. 5585258
GENERAL INFORMATION:
APPLICANT: HOUGHTON, MICHAEL
APPLICANT: CHOO, QUI LIM
TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,884
FILING DATE: 06-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/680,296
FILING DATE: 04-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CIOTTI, THOMAS E.
REGISTRATION NUMBER: 21,013
REFERENCE/DOCKET NUMBER: 22300-20100.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 2523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2523
US-08-350-884-85

Query Match 2.7%; Score 56; DB 1; Length 2523;

Best Local Similarity 100.0%; Pred. No. 1e-18; Mismatches 0; Indels 0; Gaps 0;
Matches 56; Conservative 0;

QY 292 TGCACCTGGGCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 347
DB 1000 TGCACCTGGGCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 1055

RESULT 27
US-08-440-548-85
; Sequence 85, Application US/08440548
; Patent No. 5597691
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,548
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2523
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2523
US-08-440-548-85

Query Match 2.7%; Score 56; DB 1; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTGGGCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 347
DB 1000 TGCACCTGGGCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 1055

RESULT 28
US-08-709-173-85
; Sequence 85, Application US/08709173
; Patent No. 5712145
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,173
; FILING DATE: 06-SEP-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/680,296
; FILING DATE: 04-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 22300-20100.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2523
US-08-709-173-85

Query Match 2.7%; Score 56; DB 1; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTGGGCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 347
DB 1000 TGCACCTGGGCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 1055

RESULT 29
US-08-709-177-85
; Sequence 85, Application US/08709177
; Patent No. 585799
; GENERAL INFORMATION:
; APPLICANT: HOUGHTON, MICHAEL
; APPLICANT: CHOO, QUI LIM
; APPLICANT: KUO, GEORGE
; TITLE OF INVENTION: HEPATITIS C VIRUS PROTEASE
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/709,177

;; FILING DATE: 06-SEP-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/680,296
;; FILING DATE: 04-APR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: CIOTTI, THOMAS E.
;; REGISTRATION NUMBER: 21,013
;; REFERENCE/DOCKET NUMBER: 22300-20100.20
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 813-5600
;; TELEFAX: (415) 494-0792
;; TELEX: 706141
;; INFORMATION FOR SEQ ID NO: 85:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2523 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 1..2523
US-08-709-177-85

Query Match 2.7%; Score 56; DB 2; Length 2523;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTC 347
DB 1000 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTC 1055

RESULT 30
US-08-444-818-53
; Sequence 53; Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/444,818
; APPLICATION NUMBER: US/08/403,590
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 424
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 359-3876
; TELEFAX: (508) 359-3885
; INFORMATION FOR SEQ ID NO: 85:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2523 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MEDIUM TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2523
US-08-444-818-65

;; TOPOLOGY: linear
;; MOLECULE TYPE: CDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3..5360
US-08-444-818-53

Query Match 2.7%; Score 56; DB 3; Length 5360;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTC 347
DB 1221 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTC 1276

RESULT 31
US-08-444-818-65
; Sequence 65; Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/444,818
; APPLICATION NUMBER: US/08/403,590
; PRIOR APPLICATION DATA:
; CLASSIFICATION: 424
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 359-3876
; TELEFAX: (508) 359-3885
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6785 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..6785
US-08-444-818-65

Query Match 2.7%; Score 56; DB 3; Length 6785;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 292 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTC 347
DB 1494 TGCACCTTGGCGCTCCTCGGACCTTTACCTGTCACGAGGCACGCCGATGTCATTC 1549

RESULT 32

24

US-08-444-818-74
; Sequence 74, Application, US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 74:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7310 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..7310
US-08-444-818-74

Query Match 2.7%; Score 56; DB 3; Length 7310;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACTTGGCGCTCTCGGACCTTACCTGTCACGAGGACCGCGATGTCATCC 347
Db 2019 TGCACTTGGCGCTCTCGGACCTTACCTGTCACGAGGACCGCGATGTCATCC 2074

RESULT 33
US-08-444-818-88
; Sequence 88, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 8316 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..8316
US-08-444-818-88

Query Match 2.7%; Score 56; DB 3; Length 8316;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACTTGGCGCTCTCGGACCTTACCTGTCACGAGGACCGCGATGTCATCC 347
Db 3025 TGCACTTGGCGCTCTCGGACCTTACCTGTCACGAGGACCGCGATGTCATCC 3080

RESULT 34
US-08-444-818-137
; Sequence 34, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANBV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885

137

INFORMATION FOR SEQ ID NO: 137;
SEQUENCE CHARACTERISTICS:
LENGTH: 997 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..8985
US-08-444-818-137

Query Match 2.7%; Score 56; DB 3; Length 9987;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 347
Db 3367 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 3422

RESULT 35

US-08-444-818-122
Sequence 122, Application US/08444818
Patent No. 6150087

GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANEV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 9185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-444-818-122

Query Match 2.7%; Score 56; DB 3; Length 9185;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 347
Db 3686 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 3741

RESULT 36

US-08-444-818-123/c
Sequence 123, Application US/08444818
Patent No. 6150087

GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANEV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/403,590
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 9185 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ANTI-SENSE: YES
US-08-444-818-123

Query Match 2.7%; Score 56; DB 3; Length 9185;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 347
Db 5500 TGCACCTTGGCGCTCTCTCGGACCTTTACCTGGTCAAGGACGCGCGATGTCATTC 5445

RESULT 37

US-08-444-818-176
Sequence 176, Application US/08444818
Patent No. 6150087

GENERAL INFORMATION:
APPLICANT: Chien, David Y.
APPLICANT: Rutter, William J.
TITLE OF INVENTION: NANEV Diagnostics and Vaccines
NUMBER OF SEQUENCES: 777
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,818
FILING DATE: 14-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA: US/08/403,590
APPLICATION NUMBER: 33,895
FILING DATE: 14-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Harbin, Alisa A.
REGISTRATION NUMBER: 33,895
REFERENCE/DOCKET NUMBER: 0110.002
TELEPHONE: (508)359-3876
TELEFAX: (508)359-3885
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 9379 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: misc_feature
LOCATION: 345
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is A or G"
OTHER INFORMATION: at this position which is A or G"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 351
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is T or C"
OTHER INFORMATION: at this position which is T or C"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 846
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is A or G"
OTHER INFORMATION: at this position which is A or G"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1319
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is A or G"
OTHER INFORMATION: at this position which is A or G"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2126
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is A or C"
OTHER INFORMATION: at this position which is A or C"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3659
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is C or T"
OTHER INFORMATION: at this position which is C or T"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3689
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is G or C"
OTHER INFORMATION: at this position which is G or C"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4146
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is C or T"
OTHER INFORMATION: at this position which is C or T"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4680
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is G or A"
OTHER INFORMATION: at this position which is G or A"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9080
OTHER INFORMATION: /note= "A heterogeneity may exist at this position which is A or G"
OTHER INFORMATION: at this position which is A or G"

OTHER INFORMATION: at this position which is A or G"
US-08-444-818-176
Query Match 2.7%; Score 56; DB 3; Length 9379;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTTGGGCTCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATTC 347
DB 3686 TGCACCTTGGGCTCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATTC 3741
RESULT 38
US-09-388-874-1
; Sequenced Application US/093888974
; Patent No. 6284249
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/388,874
; CURRENT FILING DATE: 1999-09-02
; EARLIER APPLICATION NUMBER: PCT/FR98/00448
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 97/02,887
; EARLIER FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9379
; TYPE: DNA
; ORGANISM: Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (320)...(9352)
US-09-388-874-1

Query Match 2.7%; Score 56; DB 3; Length 9379;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTTGGGCTCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATTC 347
DB 3686 TGCACCTTGGGCTCTCTCGGACCTTTACCTGTGTCACGAGGACGCGGATGTCATTC 3741
RESULT 39
US-09-916-359-1
; Sequence 1, Application US/09916359
; Patent No. 6538123
; GENERAL INFORMATION:
; APPLICANT: Veronique Barban
; TITLE OF INVENTION: VACCINE COMPOSITION FOR PREVENTING OR
; FILE REFERENCE: PMCF97-03A
; CURRENT APPLICATION NUMBER: US/09/916,359
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 09/388,874
; PRIOR FILING DATE: 1999-09-02
; PRIOR APPLICATION NUMBER: 97/02,887
; PRIOR FILING DATE: 1997-03-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 9379
; TYPE: DNA
; ORGANISM: Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (320)...(9352)
US-09-916-359-1

whole virus 102 (E)
sep 2001

Gene

Query Match 2.7%; Score 56; DB 4; Length 9379;
 Best Local Similarity 100.0%; Pred. No. 1e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCACCTTCGGCTCTCTGGACCTTTACTGTGTACGAGGACGCGGATGTCATCC 347
 Db 3686 TGCACCTTCGGCTCTCTGGACCTTTACTGTGTACGAGGACGCGGATGTCATCC 3741

RESULT 40
 US-07-910-760-9
 ; Sequence (9) Application US/07910760
 ; Patent No. 5683864
 ; GENERAL INFORMATION:
 ; APPLICANT: Houghton, Michael
 ; APPLICANT: Choo, Qui-Lim
 ; APPLICANT: Kuo, George
 ; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
 ; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Chiron Corporation
 ; STREET: P.O. Box 8097 (Int. Prop. R-440)
 ; CITY: Emeryville
 ; STATE: CA
 ; COUNTRY: U.S.A.
 ; ZIP: 94662-8097
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07910,760
 ; FILING DATE: 07-JUL-1992
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Blackburn Esq., Robert P.
 ; REGISTRATION NUMBER: 30,447
 ; REFERENCE/DOCKET NUMBER: 0101.002
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (510) 601-2702
 ; TELEFAX: (510) 655-3542
 ; INFORMATION FOR SEQ ID NO: 9:
 ; LENGTH: 9401 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 342..9374
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 366
 ; OTHER INFORMATION: /note= "This amino acid position
 ; OTHER INFORMATION: can also be Arg."
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 372
 ; OTHER INFORMATION: /note= "This amino acid position/
 ; OTHER INFORMATION: can also be Thr."
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 867
 ; OTHER INFORMATION: /note= "This amino acid position
 ; OTHER INFORMATION: can also be Thr."
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: 1341
 ; OTHER INFORMATION: /note= "This amino acid position
 ; OTHER INFORMATION: can also be Val."

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 2148
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Ile."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 2883
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Asn."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 3681
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Ser."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 3690
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Thr."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4167
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Leu."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4323
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Val."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4701
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Tyr."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4752
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Ser."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 5970
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Gly."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 6183
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be His."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 6186
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Cys."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 6402
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Val."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 7386
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Ser."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 7494
 OTHER INFORMATION: /note= "This amino acid position
 OTHER INFORMATION: can also be Phe."
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 7497

the virus? whole virus

OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ala."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7845
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Phe."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 8409
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Gly."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9102
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Gly."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9327
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Pro."
US-07-910-760-9

Query Match 2.7% Score 56; DB 1; Length 9401;
Best Local Similarity 100.0%; Pred. No. 18-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY 292 TGACATTCGGCGCTCTCGGACCTTTACCTGGTCACGAGGACCGCGATGTCATTCC 347
Db 3708 TGACATTCGGCGCTCTCGGACCTTTACCTGGTCACGAGGACCGCGATGTCATTCC 3763

RESULT 41
US-08-440-549-9
Sequence 9 Application US/08440519
Patent No 5712087
GENERAL INFORMATION:
APPLICANT: Houghton, Michael
APPLICANT: Choo, Qui-Lim
APPLICANT: Kuo, George
TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: P.O. Box 8097 (Int. Prop. R-440)
CITY: Emeryville
STATE: CA
COUNTRY: U.S.A.
ZIP: 94662-8097
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,519
FILING DATE: 12-MAY-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/910,760
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Blackburn Esq., Robert P.
REGISTRATION NUMBER: 30,447
REFERENCE/DOCKET NUMBER: 0101.002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2702
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 9401 base pairs

Save as before

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 342..9374
FEATURE:
NAME/KEY: misc_feature
LOCATION: 366
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Arg."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 372
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Thr."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 867
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Thr."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1341
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Val."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2148
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ile."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 2883
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Asn."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3681
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ser."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 3690
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Thr."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4167
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Leu."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4323
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Val."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4701
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Tyr."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4752
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ser."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5970
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Gly."
FEATURE:

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; NAME/KEY: misc_feature
; LOCATION: 6183
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be His."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6186
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Cys."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 6402
; OTHER INFORMATION: /note= "This amino acid position
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7386
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Ser."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7494
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Phe."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7497
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Ala."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7845
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Phe."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 8409
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Gly."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9102
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Gly."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 9327
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Pro."
; US-08-440-519-9
; Query Match 2.7%; Score 56; DB 1; Length 9401;
; Best Local Similarity 100.0%; Pred. No. 1e-18;
; Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; QY 292 TGCACITGGCGCTCCTCGGACCTTTACCTGTCACGAGGACCGCGATGTCATCC 347
; DB 3708 TGCACITGGCGCTCCTCGGACCTTTACCTGTCACGAGGACCGCGATGTCATCC 3763
; RESULT 42
; US-08-440-519-9
; Sequence 9, Application US/08440549
; Patent No. 6312889
; GENERAL INFORMATION:
; APPLICANT: Houghton, Michael
; APPLICANT: Choo, Qui-Lim
; APPLICANT: Kuo, George
; TITLE OF INVENTION: Combinations of Hepatitis C virus (HCV)
; TITLE OF INVENTION: Antigens for Use in Immunoassays for Anti-HCV Antibodies
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: P.O. Box 8097 (Int. Prop. R-440)
; CITY: Emeryville
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 94662-8097
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,549
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/910,760
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Blackburn Esq., Robert P.
; REGISTRATION NUMBER: 30,447
; REFERENCE/DOCKET NUMBER: 0101.002
; TELEPHONE: (510) 601-2702
; TELEFAX: (510) 635-3542
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9401 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 342..9374
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 366
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Arg."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 372
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Thr."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 867
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Thr."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1341
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Val."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2148
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Ile."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 2883
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Asn."
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; NAME/KEY: misc_feature
; LOCATION: 3681
; OTHER INFORMATION: /note= "This amino acid position
; OTHER INFORMATION: can also be Ser."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3690
; OTHER INFORMATION: /note= "This amino acid position
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OTHER INFORMATION: can also be Thr."
NAME/KEY: misc_feature
LOCATION: 4167
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Leu."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4323
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Val."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4701
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Tyr."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 4752
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ser."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 5970
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Gly."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6183
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be His."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6186
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OTHER INFORMATION: can also be Cys."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 6402
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Val."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7386
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ser."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7494
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Phe."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7497
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Ala."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 7845
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Phe."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 8409
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Gly."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 9102
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Gly."
FEATURE:
NAME/KEY: misc_feature

LOCATION: 9327
OTHER INFORMATION: /note= "This amino acid position
OTHER INFORMATION: can also be Pro."
US-08-440-549-9
Query Match 2.7%; Score 56; DB 4; Length 9401;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 292 TGCACCTTGGGCTCTCTGGACCTTTACCTGGTACGAGGACGCGGATGTCATTCC 347
DB 3708 TGCACCTTGGGCTCTCTGGACCTTTACCTGGTACGAGGACGCGGATGTCATTCC 3763
RESULT 43
US-08-823-895A-25
Sequence 25 Application US/08823895A
Patent No. 6433159
GENERAL INFORMATION:
APPLICANT: Kevin P. Anderson
TITLE OF INVENTION: Compositions And Methods For
TREATMENT OF HEPATITIS C VIRUS-ASSOCIATED DISEASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jane Massey Licata, Esq.
STREET: 66 E. Main Street
CITY: Marlton
STATE: NJ
COUNTRY: USA
ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/823.895A
FILING DATE: March 17, 1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/453,085
FILING DATE: May 30, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/945,289
FILING DATE: September 10, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Jane Massey Licata
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 779-2400
TELEFAX: (609) 810-1454
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 9401
TYPE: Nucleic
STRANDEDNESS: Single
TOPOLOGY: Linear
ANTI-SENSE: NO
US-08-823-895A-25

Query Match 2.7%; Score 56; DB 4; Length 94
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 56; Conservative 0; Mismatches 0; Indels

QY 292 TGCACCTTGGGCTCTCTGGACCTTTACCTGGTACGAGGACGCGG
DB 3708 TGCACCTTGGGCTCTCTGGACCTTTACCTGGTACGAGGACGCGG

RESULT 44
PCT-US91-02225-9
Sequence 9 Application PC/TUS9102225

GENERAL INFORMATION:
 APPLICANT: HOUGHTON, MICHAEL
 APPLICANT: CHOO, QUI-LIM
 APPLICANT: KOO, GEORGE
 TITLE OF INVENTION: COMBINATIONS OF HEPATITIS C VIRUS
 TITLE OF INVENTION:
 TITLE OF INVENTION: ANTIBODIES
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 545 Middlefield Road, Suite 200
 CITY: Menlo Park
 STATE: CA
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/02225
 FILING DATE: 19910329
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: CIOTTI, THOMAS E.
 REGISTRATION NUMBER: 21,013
 REFERENCE/DOCKET NUMBER: 2300-0101.44
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 327-7250
 TELEFAX: (415) 327-2951
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9401 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 PCT-US91-02225-9

Query Match 2.7%; Score 56; DB 5; Length 9401;
 Best Local Similarity 100.0%; Pred. No. 1e-18;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 292 TGCATTGGCGCTCTCGGACCTTACTGTCACGAGGACCGCGATGTCATCC 347
 Db 3708 TGCATTGGCGCTCTCGGACCTTACTGTCACGAGGACCGCGATGTCATCC 3763

RESULT 45
 US-08-823-895A-26
 Sequence 26, Application US/08823895A
 Patent No. 6433159
 GENERAL INFORMATION:
 APPLICANT: Kevin P. Anderson
 TITLE OF INVENTION: Compositions And Methods For
 TITLE OF INVENTION: Treatment Of Hepatitis C Virus-Associated Diseases
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jane Massey Licata, Esq.
 STREET: 66 E. Main Street
 CITY: Marlton
 STATE: NJ
 COUNTRY: USA
 ZIP: 08053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 COMPUTER: IBM 486
 OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/823,895A

FILING DATE: March 17, 1997
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/453,085
 FILING DATE: May 30, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/945,289
 FILING DATE: September 10, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Jane Massey Licata
 REGISTRATION NUMBER: 32,257
 REFERENCE/DOCKET NUMBER: ISPH-0203
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (609) 779-2400
 TELEFAX: (609) 810-1454
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9416
 TYPE: Nucleic
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 ANTI-SENSE: NO
 US-08-823-895A-26

Query Match 2.6%; Score 53; DB 4; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 3.5e-17;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GTGGCCCACTGTCATGCTCCACCGGACGCGTAAGACCAAGGTCCTCCGC 650
 Db 4014 GTGGCCCACTGTCATGCTCCACCGGACGCGTAAGACCAAGGTCCTCCGC 4066

RESULT 46
 US-10-104-966-13
 Sequence 13, Application US/10104966
 Patent No. 6680954
 GENERAL INFORMATION:
 APPLICANT: Matti Sallberg
 APPLICANT: Catharina Hultgren
 TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
 TITLE OF INVENTION: METHODS OF USE THEREOF
 FILE REFERENCE: TRIPEP.23AUSCI
 CURRENT APPLICATION NUMBER: US/10/104,966
 CURRENT FILING DATE: 2002-03-22
 PRIOR APPLICATION NUMBER: 09/705,547
 PRIOR FILING DATE: 2000-11-03
 PRIOR APPLICATION NUMBER: 60/229,175
 PRIOR FILING DATE: 2000-08-29
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 13
 LENGTH: 9416
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Hepatitis C virus sequence
 US-10-104-966-13

Query Match 2.6%; Score 53; DB 4; Length 9416;
 Best Local Similarity 100.0%; Pred. No. 3.5e-17;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 598 GTGGCCCACTGTCATGCTCCACCGGACGCGTAAGACCAAGGTCCTCCGC 650
 Db 4014 GTGGCCCACTGTCATGCTCCACCGGACGCGTAAGACCAAGGTCCTCCGC 4066

RESULT 47
 US-09-014-416-2
 Sequence 2, Application US/09014416
 Patent No. 6153421
 GENERAL INFORMATION:

13

150

4066
4066
4066

APPLICANT: Yanagi, Masayuki
APPLICANT: Bukh, Jens
APPLICANT: Emerson, Susanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: US 60/053,062
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 9599
TYPE: DNA
ORGANISM: Hepatitis C virus
US-09-014-416-2

Query Match 2.6%; Score 53; DB 3; Length 9599;
Best Local Similarity 100.0%; Pred. No. 3.5e-17; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 GTGGCCCACTGCTGCTCCACCGGCGGTAAGAGCACCAGGTCCTCCGGC 650
Db 4014 GTGGCCCACTGCTGCTCCACCGGCGGTAAGAGCACCAGGTCCTCCGGC 4066

RESULT 48
US-09-014-416-6
Sequence 6, Application US/09014416
Patent No. 6153421
GENERAL INFORMATION:
APPLICANT: Yanagi, Masayuki
APPLICANT: Bukh, Jens
APPLICANT: Emerson, Susanne U.
APPLICANT: Purcell, Robert H.
TITLE OF INVENTION: CLONED GENOMES OF INFECTIOUS HEPATITIS C VIRUSES AND
FILE REFERENCE: 20264276
CURRENT APPLICATION NUMBER: US/09/014,416
CURRENT FILING DATE: 1998-01-27
EARLIER APPLICATION NUMBER: US 60/053,062
EARLIER FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 9599
TYPE: DNA
ORGANISM: Hepatitis C virus
US-09-014-416-6

Query Match 2.6%; Score 53; DB 3; Length 9599;
Best Local Similarity 100.0%; Pred. No. 3.5e-17; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 GTGGCCCACTGCTGCTCCACCGGCGGTAAGAGCACCAGGTCCTCCGGC 650
Db 4014 GTGGCCCACTGCTGCTCCACCGGCGGTAAGAGCACCAGGTCCTCCGGC 4066

RESULT 49
US-08-811-566-1
Sequence 1, Application US/08811566
Patent No. 6127116
GENERAL INFORMATION:
APPLICANT: Rice, Charles et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th

STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/08/811,566
FILING DATE: 03-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1113-1-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9646 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-811-566-1

Query Match 2.6%; Score 53; DB 3; Length 9646;
Best Local Similarity 100.0%; Pred. No. 3.5e-17; Indels 0; Gaps 0;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 598 GTGGCCCACTGCTGCTCCACCGGCGGTAAGAGCACCAGGTCCTCCGGC 650
Db 4014 GTGGCCCACTGCTGCTCCACCGGCGGTAAGAGCACCAGGTCCTCCGGC 4066

RESULT 50
US-09-034-756-1
Sequence 1, Application US/09034756
Patent No. 6332028
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS C
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
CITY: ST. LOUIS
STATE: MO
COUNTRY: USA
ZIP: 63105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/034,756
FILING DATE: 04-May-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: HOLLAND, DONALD R.
REGISTRATION NUMBER: 35,197
REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
TELEFAX: 314-727-6092

4066
4066

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; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 9646 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-034-756-1

Query Match      2.6%; Score 53; DB 4; Length 9646;
Best Local Similarity 100.0%; Pred. No. 3.5e-17;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 598 GTGGCCCACTGCATGCTCCACCGGCGAGGTAAGAGCACCACCAAGGTCCCGGC 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4014 GTGGCCCACTGCATGCTCCACCGGCGAGGTAAGAGCACCACCAAGGTCCCGGC 4066
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Job time : 4815 secs

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OM nucleic - nucleic search, using sw model

Run on: August 19, 2004, 04:53:05 ; Search time 4815 Seconds
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Title: US-09-930-591-1
Perfect score: 2061
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size : 35

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6: em_estpl:*
7: em_estro:*
8: em_htc:*
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10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
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14: gb_est5:*
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17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vri:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
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SUMMARIES

Result	Query	
No.	Score	Match Length DB ID Description

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